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Pred. NO. 8 the number of results predicted by chance to have

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1 AX107857 LOCUS DEFINITION ACCESSION Result No. VERSION KEYWORDS REFERENCE SOURCE ORGANISM a a Ω 000 ဂ ဂ O 0 0 0 വവ 0.0 000 0000 AUTHORS TITLE AX107857 Sequence AX107857 Busse, U., Chypre, C. and Fradet, Y. Pca3 messenger rna species in benign Patent: WO 0123550-A 1 05-APR-2001; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo sapiens Homo sapiens (human) AX107857.1 Query Match 100 70 0.1 224052 9.6 198517 9.2 175577 9.2 177658 9.8 153479 9.8 162161 9.8 2308430 9.8 230234 9.8 23724 9.8 23724 9.8 23 . <u>بـ</u>ـــ 1 224052 198517 2 175577 2 177658 202983 208618 216488 128480 Length 146952 506 bp from Patent WO0123550. GI:13923249 DΒ AC124316 AC11579 AL1929582 AL1935269 AL1935269 AC017860 AC0122812 AC122812 AC132315 AC141860 AC141860 AC141860 AC122189 AC197028 AC197028 AC122189 AE0150528 AE0150528 AE0128804 AC0128804 AL161614 AC068522 HSJ520B18 AC093533 AC016174 AX107857 AL359314 AF103908 AL954849 AC108034 AC116849 AP005228 AP005229 AP005229 AC092700 AC024249 AC019313 AC109300 AC123450 AC123450 AC23717 ij SUMMARIES ALIGNMENTS DNA and malignant linear AC109025 Rattus no AC109025 Rattus no AC132315 Mus muscu AC134221 Rattus no AC0134221 Rattus no AC097028 Rattus no AC0297028 Macaca fa AB010268 Dyrococcu AB050558 Macaca fa AB010268 Dyrococcu AC012804 Drosophil AL161614 Human DNA AC068031 Homo sapi AL121978 Human DNA AC093533 Homo sapi AC018024 Homo sapi AC018024 Homo sapi AC108024 Homo sapi AC019313 Homo sapi AC019313 Homo sapi AC019313 Homo sapi AC019314 Homo sapi AC019314 Homo sapi AC019314 Homo sapi AC019317 Drosophil AC023717 Drosophil AC023717 Drosophil AC025278 Rattus no AC013557 Rattus no AC013657 Rattus no AC016557 Rattus no AC097237 Ra AF103908 Homo sapi AC124316 Mus muscu AC115779 Mus muscu AL929582 Zebrafish AL92566 Zebrafish AC087595 Oryza sat AP003451 Oryza sat AC122812 Mus muscu AX107860 AX107857 Description prostate tissues Euteleostomi; PAT Sequence Human DNA 30-APR-2001 Sequence

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AUTHORS
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                                                                                                           requests: clonerequestions replaced gi:13897374. $\psi$ \text{Connection}$ on May 16, 2001 this sequence version replaced gi:13897374. $\psi$ During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9. Connertnicted by the Sanger Center Chromosome 0 Marvince
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                                                                        Group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (15-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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RP11-108L4 is from the library R
                                                                                                   chromosome 9, constructed by the Sanger Centre
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                                                                           Further information can be found at
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
123 c 108 g 14.
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VECTOR: pBACe3.6
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9167. .9808
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                    21052.
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/note="MER46A repeat: matches 3.
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/chromosome="9"
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/mol type="genomic DNA"
                                                     20399.
                                                                                                                                                            note="L1PA2 repeat:
13779. .19033
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10719. .1094
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/note="MLT1F repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MIR repeat: matches 36. .79 of consensus"
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note="AluSq repeat:
                                                                                                                                                                                                   3003.
                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="AluSp repeat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="L2 repeat: matches 2685.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="AluJb repeat: matches 1. .305 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L1M4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="MLT11 repeat: matches 330.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="MLT1I repeat: matches 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="AluSp repeat: matches 1. .284 of consensus"
                                 note="MIR repeat:
                                                                    note="53 copies 2
                                                                                                        note="MER30
                                                                                                                                           note="L1PA2 repeat:
                                                                                                                                                                                                                note="AluSq repeat:
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                                                                                                                                                                                                                                                                                                                                                         note="LTR13 repeat: matches 308.
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                                                                                                                                                                                                                                                                                     note="MER58A repeat: matches 1.
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                    21340
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                                                                                                        repeat: matches 136. .230 of consensus"
                                                                                                                                                                                                                                                   repeat:
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                                     matches 112. .146 of consensus"
 matches 1. .310 of consensus"
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/note="MLT1B repeat: matches 1.
29408. .29719
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/note="AluY repeat: matches 1.
21979. .22174
                                                               /note="MIR repeat: 47204. .47488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="24 copies 2 mer ta 77% conserved"
26946. .27277
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25327. .25632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1MB3 repeat: matches 4603. .4791 of consensus"
22470. .22629
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27721. .28015
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55108. .55341
/note="MIR repeat:
57364. .57658
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                                                                                                                                           /note="AluSx repeat:
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                                               'note="AluSx repeat: matches 1.
                                                                                                              'note="L2 repeat: matches 2630.
                                                                                                                                                                           note="MER5A repeat:
                                                                                                                                                                                                           note="ORSL repeat: matches 218.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       note="AluSx repeat: matches 1.
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7126. .37446
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                                                                                                                                                                                    Submitted (28-OCT-1998) Urology Research Le
Hospital Nijmegen, P.O. Box 9101, Nijmegen
                                                                                                                                                                                                                               Bussemakers,M.J.G., Van Bokhover
Karthaus,H.F.M., Schalken,J.A.,
Isaacs,W.B.
                                                                                                                                                                                                                                                                                                                                                                         Bussemakers, M.J., van Bokhoven, A., Verhaegh, G.W., Karthaus, H.F., Schalken, J.A., Debruyne, F.M., Ru, N
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 5435)
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61785. .62178
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                /rpt_type=dispersed
533...697
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61302. .61714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59658. .59977
                                                                                                       /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                          /map="9q21-q22"
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                                             rpt_family="AluY"
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                                                                                                                                                                     ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 228; DB 9; 100.0%; Pred. No. 1.1e-114;
                                                                                                                                                                                                                                                 Van Bokhoven,A., Verhaegh,G.W.,
nalken,J.A., Debruyne,F.M.J., Ru
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present in 5% of cDNA clones"
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en 6500 HB,
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Birren,B., Nusbaum,C. and Lander,E.
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join(1571. .1753,1981. .2517)
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RS (Dases 1 to 224052)

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boukhgalter, B., Camaratta, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, D., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Naylor, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbe, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-MAR-2003) whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Mar 27, 2003 this sequence version replaced gi:24431740. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
                                                                                                                                                                                                                                                               Insert size: 208000; agarose-fp
Insert size: 22052; sum-of-contigs
Quality coverage: 9.4 in Q20 bases; agarose-fp
Quality coverage: 8.8 in Q20 bases; sum-of-contigs
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42641: contrig of 677 bp in length
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43862: contrig of 1121 bp in length
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53391: gap of 100 bp
57454: contrig of 2063 bp in length
57554: gap of 100 bp
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166679: contig of 21235 bp
166779: gap of 100 bp
224052: contig of 57273 bp
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126026: gap of 100 bp
145344: contig of 19318 bp
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41964: gap of 100 bp
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7: contig of 3001 bp in length
7: gap of 100 bp
8: contig of 2751 bp in length
8: contig of 4482 bp in length
0: contig of 4482 bp in length
0: gap of 100 bp
2: contig of 3892 bp in length
2: contig of 3892 bp in length
2: gap of 100 bp
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9: gap of 100 bp
9: contig of 13468 bp in length
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CE 2 (bases 1 to 198517)

RS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,

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ACI15779.5 GI:29294112
HTG: HTGS_PHASE1; HTGS_DRAFT.
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Birren,B., Nusbaum,C. and Lander,E.
Mus musculus, clone RP23-153L22
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80780. .94247
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/note="assembly_fragment"
62658. .65408
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145445. .166679
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70091. .73982
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65509. .69990
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Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Anderson,S., Arachchi,H.M., Camarata,J., Chang,J., Choe
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Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 195514 bases at least Q40

Consensus quality: 195343 bases at least Q30

Consensus quality: 196343 bases at least Q30

Consensus quality: 196340 bases at least Q30

Consensus quality: 196340 bases at least Q30

Quality coverage: 10.1 in Q20 bases; sum-of-contigs
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17449: gap of 100 bp
18521: gap of 1072 bp in length
18621: gap of 100 bp
19526: contig of 905 bp in length
19626: gap of 100 bp
7: Contig of 1601 bp in length
7: gap of 100 bp
8: contig of 2825 bp in length
8: gap of 100 bp
7: gap of 100 bp
9: contig of 5515 bp in length
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Danio rerio
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Submitted (23-APR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                           Direct Submission
                                        Dunn,
                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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87660: gap of 100 bp
166311: contig of 78651 b
166411: gap of 100 bp
198517: contig of 32106 b
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46652: gap of 100 bp
68280: contig of 21628 bp
68380: gap of 100 bp
87560: contig of 19180 bp
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Ml3 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMMIL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Repeat names beginning 'Or' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 ATTTCTTGCCTCGTATTGTCT 138
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Apr 11, 2003 this sequence version replaced gi:29786465.
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                                                                                        Submitted (11-APR-2003) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                    Almeida, J.
                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
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Zebrafish DNA sequence
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CH211-117M12 is from a CHORI-211 BAC library
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                                                                                                                   Direct Submission
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33089 c 32287 g 55347
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/db_xref="taxon:7955"
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, RMBL; Sw:, SWISSPROT; TE:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www/Projects/D_rerio/fishmask.shtml DERY-45018 is from a Zebrafish BAC library
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                                                                                                                                                                                               Diagnocure Inc. (CA)
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Pca3 messenger rna species in benign and malignant prostate tissues
Patent: WO 0123550-A 4 05-APR-2001;
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Contact: zfish-help@sanger.ac.uk
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                                            /note="oligonucleotide"
                                                                      /organism="synthetic co
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
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* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* The accession number will be preserved.

* 45288 45387: gap of unknown length

* 45288 153479: contig of 108092 bp in length.
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Oryza sativa (japonica cultivar-group)
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Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 153479)
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Oryza sativa (japonica cultivar-group) chi
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Hahn, J.-H. and Eun, M.Y.
Direct Submission
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and Eun, M.Y.
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33690 c 32999 g 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza Bativa
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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100.0%; Pred. No.
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6.7;
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ESS ***, 2 ordered pieces.
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AUTHORS
TITLE
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SOURCE
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JOURNAL
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                                                                                                                                                     gene
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                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                            Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

On Mar 12, 2002 this sequence version replaced gi:16904688. Genes were predicted from the integrated results of the following: GENSCRAN.0. BLASTW2.0 as well as SplicePredictor (October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTW2.0. ESTS represent the identified cDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative' and '-like protein. A gene without significant homology to any protein but with EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted with a gene prediction program is classified as a 'hypothetical' protein.

The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of this clone ends at the position 13,793 of P0678F11 (DDBJ: AP003437) clone at the position 148,368 to 150,019 of 3' end. The sequence of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
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Katayose, Y., Wu, J., Niimura, Y., Cheng, Z., Nagamura, Y.,

Antonio, B.A., Kanamori, H., Hosokawa, S., Masukawa, M., Arikawa, K.,

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Yamagata, H., Yamane, H., Yoshiki, S., Yoshihara, R., Yukawa, K.,

Yano, M., Jiang, J. and Gojobori, T.

The genmence and structure of rice chromosome 1
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (28-MAR-2001) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The genome sequence and structure of rice chromosome Nature 420 (6913), 312-316 (2002) 22337376
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                                                                                                                                                                                                                                              /cultivar="Nipponbare"
                                                                                                                                                  join(1042.
                                                                                                                                                                                                                                                                             organism="Oryza sativa
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                                                                                                                                                                                                                              db_xref="taxon:39947"
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gene

SdC

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trānslation="MEQLRTIGRELAMGSQGGWGQSKEFLDLVKSIGEARSKAEEDRI ISRELDHLKRRLADPUVRRKWELLLRLVYAEMLAHASFGHHAVKWTHDESLPKI ISRELDHLKRRLADPUVRRKWELLLRLYYAEMLAHDASFGHHAVKWTHDESLPVLK RITSYLAVSLELDERHDLVILVVAITIQKDLRSUNTLVVQGHAAFTAACRLIGEGATPAVLK RITSYLAVSLEDHDVRKKAVMALHRFYQRSPSVSHLVSNFRKRLCDNDPGVMGATLCPL YDLILLBDPNSYKDLVVSFVNILKQVAERRLFTSYDYHQMPAPFIQIKLLKILAVLGSG DKQASGNMYMVLGDIRRKGDTASNIGNALLYENGICICISISIFPNAKMLDAAAFTTSKFLKSDSKASGNMYMVLGDIRKRGDTASNIGNALLYENGICICISIFPNAKMLDAAAFTTSKFLKSDSHNLKYMGIDALGRLIKINPDIAEBHQLAVIDCLEDPDDTLKRKTFELLYKMTKSTVLYVAMTKSTVAMTKSTVAMTKASTVAMTKASTLKINPDIAEBHQLAVIDCLEDPDDTLKRKTFELLYCMTKSTVAMTKASDLIVINGESMINITDHHYKTELASRCUELAEQRAPSNOMFICYMKVEBHAGDLVNIRVAHNLABGFGEEDEGADSQLRSSADDSYLLYGARKLDMLPEGENGGALTMANARTTSKFLKGALGALGCASTANASTTSCASTIGKLTDLPEGADSQLRSSADDSYLLSFLNGCSCASTANASTTSCASTIGKLTDLPEGADSQLRSSADDTSTANASTTSCASTIGKLTDKLPEGADSGLRSSADDTSTANASTTSCASTIGKTLTDKLPEGADSGLRSSADDTSTANASTTSCASTIGKTLTDKLPEGADSGLRSSADDTSTANASTTSCASTIGKTLTDKLPEGADSGLRSSADDTSTANASTTSCASTIGKTTSTANASTTSCASTIGKTTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTSTANASTTSCASTIGKTST
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19173. .19289,19376. .19432,19943. .20074,20176. .20373,
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20815. .20925,21021. .21236,21330. .21515,22041. .22643)
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DGGERDRSYSNYGGYGNNEGYSSAPSGYNPYNNGGGYGGSYGGGSYNGGGYGGSTYONG
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TQPGSSSGQNENSGERRDNGGGGGGRNGLFGPTFQAVGGYMDRRFGFD"
COMPLEMENT (JOIN (10814. .11478,13318. .13418,14749. .14934,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /proteIn id="BAB86129.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FNACVSEKSTALAVLDPSGMMNSSGRSFSGSSYSNSSTDTYGSGGRQQQQQQQQYEAA
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GGYGYNGGYNAGSVTLYGAGVGTPYYGGGGGGGYTGGGSVPYGGGGGVPAGYMTPQNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="contains EST AU068098(C11856)
unknown protein"
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unknown protein"
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YGGNSGNPINIYYGSSTGVVAGSGSYYGGGGYGGGITSYGGSLSYGKDGGYGGSNSPY
GGGSSIIISGAAPIPHNNFGGGGTGWPVPPPPQDGGSGAAPVFIRAEEVKVIYHHTPP
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complement (4165. .5010)
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/protein_id="BAB86130.1"
/db_xref="GI:19386749"
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complement/7/77
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    YVQQAIENGAAPYIPESERSGVVSVGNYKAQDQQETSAHALRFEAYELPPAASQASIS
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/note="h-----
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gene

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132589 CCACTACCGATTTTCTATTT 132570
1 (bases 1 to 208430)
McPherson, J.D. and Watto
                                                                                                                                          Mus musculus
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                       AC122812 208430 bp DNA 1
Mus musculus chromosome 1 clone RP23-285M9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCACTACCGATTTTCTATTT 121
        sequence of Mus musculus clone
                                                                                                                                                                       musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MEGGGGHAPTPGVCRYPAGGSPFAASGRPRICPGGVARLDGKQE EPQERAPSELSCSGSSVDCRRRRNPSLRRGGGAEPSEGAEPAPPPATTPPVL" join(32933. .33059,33753. .33948,34052. .34279,34608. .34839,34927. .35034,35147. .35419,35712. .35996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVVNYASFEIDYLFVSWS"
join(28678 . .28714,29296 . .29459,29480.
/gene="P0413CO3.7"
join(28678 . .28714,29296 . .29459,29480.
/gene="P0413CO3.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /traiblation="moratillhnppclsltwmlgvhnqirqlmkfptimivqqtlnl
LSKRLFfvnrqakatieptqygedllsnrrnpnalkehllkmtaehankrgkpl
Hadngnveigngygegdkrkdiahkakkgadlfbetlrqrlarrgilkdeatnnrft
Ikqnvdspygqipegdkrkdiatakkgadlfbetlygngtgttqwdrpapaplntmqhq
Ikqnvdspygqikaaqelppgwyexhtntgasyfyngstgttqwdpdapaplntmqhq
Appssslfbenmeeallostggkyyxntntqatqmepptavneovaphaptnaavemaa
Qntdiwnsqmqrclgggwguglvqbwgycnhctrvqnlpfqqvpsypnntthsssnk
Npgnvaakdrssakpffgkanrkdhrkrnrfeddeldpmdpssysdaprrggwymiffi
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26050. .26215,26559. .26612,26978. .27108,27228. .27269,
27975. _28053,28156. .28234,28437. .28597))
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27975. .28053,28156. .28234,28437. .28597))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34927. .35034,35147. .35419,35712. .35996)
/gene="p0413C03.8"
/note="contains ESTS
AU065676(E50933),D24223(R1545),AU030352(E50933)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="hypothetical protein
similar to Arabidopsis thaliana chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKGPSLQDALQKDAAARQVGVTPTGNNPILFKDLLG"
complement(join(24745. . . 24946, 25096.
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SSSTSSQQATNGGVSSEVGGSTSSQARESTYGSKRQQATEVSAEKQRLAASLFGKADR
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TQLEGLLGPASASPVVSETPASSTSKTPDLMSI FSDDVQTGVTSGSTEPSLGVNVVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="MAAAANGAACCGGATGPGYATPLEAMEKGPREKLLYVTCVYNGT/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="putative selenium binding protein"
protein_id="BAB86133.1"
db_xref="GI:19386752"
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/db_xref="GI:19386750"
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                                                                                                                                                                                                                                  GI:22748565
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                                and Waterston, R.H.
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Pred. No. 6.6;
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Muzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anyalbechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Bahay, C., Burch, P., Burreil, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Clecko, J., Chavez, D., Chen, G., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davab, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Drager, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93902 TACCGATTTTCTATTTCTTG 93921
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On Sep 6, 2002 this sequence vers
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Parkway, St. Louis, MO 63108, USA
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McPherson, J.D. and Wat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED Rattus norvegicus (Norway rat)
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McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: M_BA0285M09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC109025.5 GI:25139227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC109025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----- Project Information ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61643 a
                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 215616)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6, 2002 this sequence version replaced gi:22475552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/db_xref="taxon:1000"
/chromsome="1"
/clone="RP23-285M9"
a 40063 c 41477 g 65247 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.8%; Score 20; DB 100.0%; Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Center -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 208430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTG 20-NOV-2002
IN PROGRESS
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REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

Center project name: GPRH Center clone name: CH230-276A24 Center Summary Statistics Assembly program: Phrap; version 0.990329 Consensus quality: 181529 bases at least Q40 Center: Baylor College of Medicine Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu

Project Information

REFERENCE

JOURNAL

TITLE

AUTHORS TITLE

JOURNAL

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Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garram, M., Ganter, T., Haland, P., Haland, R., Gardy, M., Gerrand, M., Ge
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FEATURES

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Query Match
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                                                                                                                                                                                                                                                                                                                                                           Mus musculus chromosome UNK clone RP24-234J3, WORKING DRAFT SEQUENCE, 11 unordered pieces.
AC132315
AC132315.1 GI:22657777
AC132315.1 GI:22657777
HTG; PH3CE_IHTGS_DRAFT; HTGS_FULLTOP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20;
Submitted (03-SEP-2002) Genome Sequencing Center, 4444 Forest Park
                                                            2 (bases 1 to 230279) McPherson, J.D. and Wat
                                  Direct Submission
                                                                                                                                                                             1 (bases 1 to 230279)
McPherson, J.D. and Wat
                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC132315
                                                                                                                    The sequence of Mus musculus clone Unpublished
                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 215616: contig of 215616 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGTGCTTTATAAAGCACTC 30565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAGTGCTTTATAAAGCACTC 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 end_sequence:BZ161263"
52149 a 44056 c 42561 g 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 183677 bases at least Q30 Consensus quality: 185417 bases at least Q30 Estimated insert size: 185302; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="wgs_contig"
complement(212205.
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114,05. .12230
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clone_end:Sp6"
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clone_end:Sp6"
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/mol_type="genomic DNA"

/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        one_end:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1067
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.8%; UT
100.0%; Pr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence:BZ161264"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .10254
                                                            and Waterston, R.H.
                                                                                                                                                                                    and Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230279 bp
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                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Insert size: 196000; agarose-fp
Insert size: 228189; sum-of-contigs
Quality coverage: 17.24 in Q20 bases; agarose-fp
Quality coverage: 11.34 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: M13; 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site:http://genome.wustl.edu/gsc/index.shtmlContact: submissions@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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59107
59207
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                                                                                                                                                                                                                                                                                                         /note="assembly_name:Contig11"
372. .1190
                                                        /note="assembly_name:Contig21"
13017 .32164
                                                                                                                                                 /note="assembly_name:Contig20"
                                                                                                                                                                                                                                                /note="assembly_name:Contig14"
1291. .2555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol
                      note="assembly_name:Contig22
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                                                                                                                                                                                                             note="assembly_name:Contig16"
                                                                                                                                                                                                                                                                                                                                                                                                 clone="RP24-234J3"
                                                                                                                                                                                                                                                                                                                                                                                                                                    chromosome="UNK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector: plasmid; 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59206: gap of unknown length
88462: contig of 29256 bp in 1
88562: gap of unknown length
134957: contig of 46395 bp in 1
135057: gap of unknown length
170399: contig of 35342 bp in 1
170499: gap of unknown length
230279: contig of 59780 bp in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          l_type="genomic DNA"
_xref="taxon:10090"
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59106: contig of 26842 bp in length
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contig
gap of
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gap of unknown length
contig of 1265 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of 271 bp in length gap of unknown length
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of 1531 bp in length
unknown length
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unknown length
of 19148 bp in lengt
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JOURNAL REFERENCE REFERENCE AUTHORS TITLE

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VERSION KEYWORDS

ORGANISM

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AC141860/c
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                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contilly has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Akhter.N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S. Cariaga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B., Margulies, B.H., Masiello, C., Maskeri, B., McDowell, J., Paguirigan, C., Pearson, R., Portnoy, M.E., Prasad, A., Paguirigan, C., Pearson, R., Schueler, M.G., Sison, C., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L., Wetherby, K.D., Wiggins, L., Young, A. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archosauria; Aves; Neognathae; Craniata; Vertebrata; Euteleostomi; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC141860.2 GI:29501863
HTG; HTGS PHASE2; HTGS DRAFT.
Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC141860 237234 bp
Gallus gallus clone TAM31-57D16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AAGTGCTTTATAAAGCACTC 22
                                                                                                                                                                                                                                                                                                               Submitted (03-APR-2003) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Apr 3, 2003 this sequence version replaced gi:29124110.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (19-MAR-2003) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 237234)
                                                                                                                                                                                                                                                                                                                                                                                                                               Green, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pieces
                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inpublished
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                                                                                                                                                      Web site: http://www.nisc.nih.gov
contact: nisc zoo@nhgri.nih.gov
------ Project Information
Center project name: dft
Center clone name: 057D16
                                                                                                                                                                                                                                                                      Center: NIH Intramural Sequencing Center Center code: NISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_name:Contig24"
88563 . 134957
/note="assembly_name:Contig25"
135058. .170399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_name:Contig23" 59207. .88462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_name:Contig27"
53964 c 52004 g 59749 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170500. .230279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ω
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WORKING DRAFT SEQUENCE, 10 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 230279; 6.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * consists of 10 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 12818 12917; contig of 12817 bp in length

* 12918 85073; contig of 72156 bp in length

* 85174 88714; contig of 3541 bp in length

* 85174 88714; gap of unknown length

* 85174 88714; gap of unknown length

* 85175 11928; contig of 55114 bp in length

* 85176 11928; contig of 55114 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated contigs have been trimmed away, and each base is associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200290
200390
211977
2112077
2121446
214246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            191668
191768
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113929
114029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert size: 180000; agarose-fp
Insert size: 236334; sum-of-contigs
Quality coverage: 11.59x in Q20 bases; agarose-fp
Quality coverage: 8.83x in Q20 bases; sum-of-conti
  /note="assembly_fragment"
212077. .214145
                                                                                                                                                                                                                                                                                                                         12918.
                                                                                                                                                                                                                                                                                                                                 vector_side:left"
1291A aso77
                                                                                                                                                                                                                                                                                                                                                                             clone_end:T7
                                                         200390
                                                                                                                                                                                                                   88815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                            /note="assembly_fragment"
114029. .191667
                                                                                                                                                                                                                                 note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic_DN
/db_xref="taxon:9031"
/clone="TAM31-57D16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Gallus gallus"
                                                                                                           191768. .200289
                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_
                                                                             note="assembly_fragment"
                                                                                                                                 note="assembly_fragment"
                                                                                                                                                                                                                                                                                           note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191767: gap of unknown length
200289: contig of 8522 bp in length
200389: gap of unknown length
211976: contig of 11587 bp in length
212076: gap of unknown length
214145: contig of 2069 bp in length
214245: gap of unknown length
2242424: gap of unknown length
224294: gap of unknown length
224294: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .237234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          lib="TAM31"
                                                                                                                                                                                                                                                                          .88714
                                                                                                                                                                                                                                                                                                                            .85073
                                                                                                                                                                                                                      .113928
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/note="assembly_fragment" 214246. .224194

'note="assembly_fragment"

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AUTHORS
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AC134221/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
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Allen, C., Allen, H., Alsbrooke, S., Amin, A., Anguiano, D.,
Allen, C., Allen, H., Alsbrooke, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, B., Baden, H.,
Baladwin, D., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, B.,
Cardenas, V., Carter, K., Cavazos, I., Ceasax, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M.L., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Ganca, R., Garcia, A., Garrer, T., Garza, M.,
Gebregeorgis, B., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hogues, M.,
Hellins, B., Howells, S., Hulyk, S., Hume, J., 1dlebird, D., Jackeon, A.,
Jackeon, L., Jacob, L., Jebow, H., Levan, J., Levis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensuthewa, L., Coulesged, H., Lozado, R.J., Lu, X., Ma, J.,
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Mangum, B., Mapus, P., Martin, K., Martin, R., Montemayer, J., Moore, S.,
Norgan, M., Morris, K., Morris, S., Montemayer, J., Morris, S.,
Norris, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Plopper, F., Seiter, A., Popoic, D., Primus, E., Pu, L., L.,
Shetty, J., Shartsbern, A., Sesen, J., Sose, R., Raijs, R.,
Reilly, B., Sodetgren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 GTTTCTATCCTTCCTACTCA 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Norway rat)
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clone_end:SP6
vector_side:right"
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; Pred. No
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REFERENCE
AUTHORS
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TITLE
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On Nov 13, 2002 this sequence version replaced gi:23306103.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence rontigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Bstimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Caps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be preserved
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Consensus quality: 221775 bases at least Q40
Consensus quality: 224525 bases at least Q30
Consensus quality: 226115 bases at least Q30
Consensus quality: 226115 bases at least Q20
Estimated insert size: 226851; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                              135351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                      135251
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                                                                                                                                      /clone="CH230-1005"
87008. .89104
/note="wgs_contig"
139028. .141263
                                                                 135351.
                                                                                                                                                                                                   /organism="Rattus norvegicus'
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                          1 135250: contig of 135250 bp in length
1 135350: gap of unknown length
1 238817: contig of 103467 bp in length.
Location/Qualifiers
                                                             /note="wg8_contig"
|35351. .136555
                                                                                                                                                                                                                                                                                                                .238817
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Gobter, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Gazza, M., Gebregeorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindarine, M., Martin, R., Martine, M., Mahindarine, M., Morte, S., Morris, K., Morris, S., Murche, S., Murche, S., Morris, K., Martine, S., Murche, S., Mair, L., Mair, L., Martine, Martin
                                                                                      Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Puszo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Puszo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Shetty, J., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Sneed, A., Sdergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Sneed, A., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J.,
Wallson, R., Walzer, R., Wooden, H., Worley, K.,
Williagn, R., Wallson, R., Wleczyk, R., Wooden, H., Worley, K.
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           Williams,G., Wills
Wright,D., Wright,
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Allen,C., Allen,H., Alsbrooks,S., Amin,A., A
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100.0%; Prr
willson,R., Wleczyk,R., Wooden,H., Worley, right,R., Wu,J., Yakub,S., Yen,J., Yoon,L.,
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                                                         Worley, K
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submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 10, 2003 this sequence version replaced gi:23264500. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (06-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.)
NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the accession number will be preserved.
1 243174: contig of 243174 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              provided by the submittor.
This sequence will be replaced
by the finished sequence as soon as it is available and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is believed to be correct as given, he of the gaps between them are based on
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Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: GGXU
Center clone name: CH220-93J21
Center clone name: CH220-93J21
Center clone name: CH220-93J21
Consembly program: Atlas 3.0;
Consensus quality: 234402 bases at least Q40
Consensus quality: 236580 bases at least Q30
Consensus quality: 236580 bases at least Q30
Consensus quality: 236580 bases at least Q30
Consensus quality: 237637 bases at least Q20
Estimated insert size: 243918; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: hgsc-help@bcm.tmc
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Center code: BCM
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end_sequence:BH327070"
complement(240473...24
                                                                           site:EcoRi
                                                                                                                     clone
                                                                                                                                                                                                                           /note="wgs_end_extension
clone_end:T7"
                                                                                                                                                                                                                                                                                                                                                                                                      organism="Rattus norvegicus"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-OCT-2002) Genome Sequencing Center, Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 247309) McPherson,J.D. and Waterston,R.H.
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McPherson, J.D. and Wat
Direct Submission
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On Oct 17, 2002 this sequence version replaced gi:23683310.
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Parkway, St. Louis, MO 63108, USA
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Submitted (17-OCT-2002) Genome Sequencing Center, 4444 Forest
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                       Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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/db_xref="taxon:10090"
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a 47853 c 48954 g 77992
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                                                                                                                                                                                                                                                                                                                                                                                                             Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
                                                                                                                                                                                                 19;
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Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
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Macaca fascicularis brain cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirai, M., Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K.
              AE010268.1
                        genome.
AE010268 AE009950
                                                       Pyrococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (25-OCT-2000) Katsuyuki Hashimoto, National Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                                  /tissue_type="brain parietal lobe"
/clone_Tib="macaque brain cDNA lib
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/dev_stage="adult"
402 g 489 t
                                                                                                                                                                                                                                                                                                                                                       organism="Macaca fascicularis"
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                                                       10084 furiosus DSM 3638,
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SOURCE

Pyrococcus furiosus DSM 3638

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Divergence of the hyperthermophilic archaea Pyrococcus furiosus P. horikoshii inferred from complete genomic sequences
Genetics 152 (4), 1299-1305 (1999)
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Robb.F.T., Maeder,D.L., Brown,J.R., DiRuggiero,J., Stump,M.D.,
Yeh,R.K., Weiss,R.B. and Dunn,D.M.
Genomic sequence of hyperthermophile, Pyrococcus furiosus:
implications for physiology and enzymology
Meth. Enzymol. 330, 134-157 (2001)
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Archaea; Euryarchaeota; Thermococci; Thermococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-FEB-2002) Human Genetics, University of Utah, South 2030 East, Salt Lake City, UT 84112, USA Location/Qualifiers
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LKEMESAKKSGDSVGGVVEVVAINVPPGLGGPYEDDIEADLASTFFRIPAVKGVEFGL
GFKVSEKRGSEVNDPYVIKNGEIQTVTNNHGGIIGGITTGMPIVARIAFKPTPSIYLP
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YTTGAPITVIVENKDVDSSYYEEIKDFPRPGHADYPAKIKYFGFNDYRGGGRFSGRTH
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68. .1078
                                                                                                                      /protein_id="AAL81825.1"
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Aromatic amino acid family"
/codon start=1
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Aromatic amino acid family; (aroC)"
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Aspartate family; (aspB-2)"
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1145. .1375
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1359. .2396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="PF1700"
/EC_number="4_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mol_type="genomic DNA"
strain="DSM 3638"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      furiosus
                                                                                                                                                                                                                                                                                 Amino Acid Biosynthesis:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brown,J.R.
cus furiosus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSM 3638"
                        Acid Biosynthesis:
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                                                                                                                                                                                                                                                               CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="PF1703"
2381 . 2827
/gene="PF1703"
/EC_numbe-
                                                                                                                                                                                                                                          complement (3883. .5049)
/gene="PF1706"
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/note="Function Code: 1.2 A
Aromatic amino acid family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aromatic amino acid family"
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/db_xref="GI:18893869"
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/note="Function Code: 1.2 Am
Aromatic amino acid family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (3144. .3890)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (3144. .3890)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="hypothetical
/protein_id="AAL81828...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VASVHPMFGPGAKSFRGHLFYRCPCKGQGKRRRRCRKVYRRIGGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                   complement (3883. .5049)
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/protein_id="AAL81829.1
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/transl_table=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="PF1705"
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/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene="PF1704"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="
                                                                                                                                                                                                                                                                                   'gene="PF1706"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                          synthetase alpha subunit"
9.1"
                                                                                                                                                                                 Amino Acid Biosynthesis: y; (trpB-2)"
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VABEKGIKLISDEIYABISFKSFFDYBELYBNTVTVKGPSKLVSMTGFRLGYAIADKE
EIRKIKTFIESTVTCVPPFVQRAGIKALELRDELMKKVSREYKRRABLASKILRGLEF
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/trānslation="mwfgefggqyvpetlieplkelekaykrfkddeefnrqlnyylk Twagrptplyyakrltekiggakiylkredlvhggahktnnaigqallakfmgktrli aetgagqhgvatamagallgmkydiymgaedverqkwnvfrmkllganvipvnsgsrt LKDAINEALRDWVATFEYTHYLIGSVVGPHPYPTIVRDFQSVIGREAKAQILEAEGQI

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DEFINITION
ACCESSION
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ORGANISM
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                        AUTHORS
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                                                                                                                               HTG; HTGS_PHASE2.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
                                                                                                                                                                                                                           Drosophila melanogaster, AC012804
AC012804.1 GI:6223516
Submitted (03-NOV-1999) Celera Genomics,
                                                         Neoptera, Endopterygota, Diptera, Brachycera, Ephydroidea, Drosophilidae, Drosophila. (bases 1 to 13588)
                                      Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                 AC012804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.3%; Score 19; DB 1; Length 10084; Similarity 100.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                   GCTTTATAAAGCACTCAAT 7284
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTTTATAAAGCACTCAAT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                        Submission
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MLSYFLQDEEGQIKPTHSIAPGLDYPGVGPEHAYLKKIQRAEYVTVTDEEALKAFHEL
SRTEGIIPALESAHAVAYAMKLAKEMSRDEIIIVNLSGRGDKDLDIVLKVSGNV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (6230. .7528)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IIISPGPGHPLDRREVGNSPEIVLESEVPLLGVCLGHQIIGAVFGGKIGRVTPKHGKA
SLIRHDGKGVYRGLDNPFLAGRYHSLAVLEPPKGPKVTSVSLDDGVIMGIRHKTLPIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Function Code: 1.2 Amino Acid Biosynthesis:
/romatic amino acid family; (trpG)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (5662. .6228)
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Aromatic amino acid family; (trpF)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (5036. .5662)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="anthranilate synthase
/protein_id="AAL81833.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (6230. .7528)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="anthranilate synthase component II"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="phosphoribosyl anthranilate isomerase'
/protein id="AAL81831.1"
/db_xref="GI:18893870"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /EC_number="4.1.3.27"
/note="Function Code: 1.2 Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="PF1709"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MLIKELDRVSPLRLYLILRQLEYPFILMSAEKHSKKARFTYLSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             romatic amino acid family"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MILIINNRDSFVWNLAEYVSFFDEAVVVSNKITLSEVKKLDPDG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MFVKICGIKSLEELEIVEKHADATGVVVNSNSKRRIPLEKAREI"
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45 West Gude Drive,
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                                                                                                               Muscomorpha;
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JOURNAL
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                                                                                                                                                                                                                                          Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Mardonald, P., Marquis, N., McCerthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Oliver, J., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vassiliev, J., Zainoun, J., Zimmer, A. and Zody, M.
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This sequence was identified as CDM:10210414
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                                                                  Research, 320 Charles Street, Cambridge, MA 02141, US All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boukhgalter,B., Brown,A., Burkett,G., Boukhgalter,B., Brown,A., Burkett,G., Collins,S., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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* NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                  Submitted (27-APR-2000) Whitehead Institute/MIT Center
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                               Direct Submission
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by the finished sequence as soon as it is
the accession number will be preserved.
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                     Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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* NOTE: This record contains 65 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
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----- Project Information
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                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cambridgeshire, CB10 ISA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@ganger.ac.uk
On Nov 15, 2001 this sequence version replaced gi:15304689.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30), an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em. KMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
database can be found at
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                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr13 RP11-346fll3 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                   IMPORTANT: This sequence is not the entire insert of clone RP11-346L13 It may be shorter because we sequence overlappi sections only once, except for a short overlap. The true left end of clone RP11-471M10 is at 68947 in this sequence. The true right end of clone RP11-181D10 is at 200
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Human DNA sequence from clone RP11-346L13 on
13q14.3-21.31, complete sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                  http://www.chori.org/bacpac/home.htm
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/clone="RP11-360N22"
/clone_lib="RPCI-11 |
/organism≃"Homo sapiens"
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2 (bases) to 146952)

RS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
Anderson,S., Baldwin,J., Barna,N., Burkett,G.,
Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G.,
Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L.,
Klein,J., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J.,
Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Marquis,N.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R.,
Meddrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
McMarin,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J.,
Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
O'Neil,D., Olivar,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Pisani,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Teefaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J.,
Piret, Submission,J., Zimmer,A. and Zody,M.,
Direct Submission,J., Zimmer,A. and Zody,M.
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  Birren, B., Linton, L., Nusbaum, C., 1
Anderson, S., Barna, N., Bastien, V.,
                                                    Submitted (03-MAY-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 146952)
                                                                                                                                            Direct Submission
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Birren, B., Linton, L., Nusbaum, C.
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HTG.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (human)
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/note="Single clone region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Restriction digest data confirm the assembly. 15606 \text{ c} 15147 \text{ g} 19688 \text{ t}
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Pred. No.
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ne 8, clone RP11-23K11, compl
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25;
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Lander, E., Ali, A., Allen, N, Bloom, T., Boguslavkiy, L.,
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                             Allen, N.,
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REFERENCE
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A (bases 1 to 146552)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Alderson, S., Barna, N., Bastien, V., Blom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cock, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Perreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meddrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phuhkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Fieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Venng, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
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MacLean, C., Macdonald, P., Major, J., Marquis, N., Mathews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Mihova, T., Melerson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Raymond, C., Reetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,
Seaman, J., Rosetti, M., Roy, A., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (30-MAY-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 30, 2002 this sequence version replaced gi:20331012. All repeats were identified using RepeatMasker: All F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: L7815
Center clone name: 23_K_11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center code: WIBR
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Center: Whitehead Institute/ MIT Center for Genome Research
   /clone="RP11-23K11"
/clone_lib="RPCI-11 Human Male BAC"
/complement (255. .413)
/rpt_family="MIR"
417. .474
                                                                                                                                                                                                                                        /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                      map="8"
                                                                                                                                                                                                     chromosome="8"
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                                  /rpt_family="THE18-int"
complement(24454. .2476)
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/rpt_family="MIR"
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/rpt_family="Alusx"
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                                                                                                                                                                                                                                                                                                             complement (23151.
                                                                                                                                                                                                                                                                                                                                            complement(22803, .23068)
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                           complement (20389. .20507)
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (16884
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. .4596
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                                                                                                                                                                                                                                        family="L1ME3A"
. .23510
                                                                                                                                                                                                                                                                                                                                                                                                                                                 family="FRAM"
ement(?^^^
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. .1816^
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ement (1501)
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lement(12690. .12
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lement(2397..2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family="AluSp"
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                                                                                                                                                                                                                                            The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at the WORMPEP database can be found at the Hollow and the WORMPEP database can be found at the WORMPEP database can be found contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143385 bp DNA linear PRI 31-UUL-20 Human DNA sequence from Clone RP3-520B18 on chromosome 6p24.1-25. Contrains the 5' end of FARSI (phenylalanine-tRNA synthetase), a pseudogene similar to microtubule-associated protein 1A/1B light chain 3, a CpG island, ESTs, STSs and GSSs, complete sequence.
                                                                                                                                            Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 RP3-520B18 is from the library RPCI-3 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             requests: clonerequest@sanger.ac.uk
On Jun 4, 2000 this sequence version replaced gi:8247028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (27-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL121978.5 GI:8247628
HTG; CpG island; tRNA synthetase.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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complement(26647. .26752)
/rpt family="L2"
27726. .27924
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26619. .26646
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                                                                           Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
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100.0%; Pred. No. 24,
tive 0; Mismatches
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1980. .5628
/note="L11A8 repeat: matches 5514. .6163 of consensus"
                 /note="L2 repeat: matches 1545.
complement(21298. .21740)
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                                                                                                                                                                 /note="L2 repeat: matches 2178.
20794. .21288
                                                                                                                                                                                                  19884. .19966
/note="L2 repeat:
20286. .20497
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/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluSq repeat: matches 1. .287 of consensus"
17250. .17555
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                                                                                                                                                                                                                                                                          note="MER47A repeat: matches 2.
19573. .19646
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                                                                                                        note="MIR repeat:
                                                                                                                                                                                                                                                                                                                                                                note="match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               6921. .17206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="AluY repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6119. .16241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="MIR repeat: matches 131.
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                                                                                                                                                                                                                                                                                                                               note="match:
                                                                                                                                                                                                                                                                                                                                                                                                      note="AluYb8 repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="L2 repeat: matches 2629. .2750 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="FLAM_A repeat: matches 1.
                                                                                                                                                                                                                                                       note="37 copies 2 mer at 83% conserved"
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Em: AQ129989"
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                                                 /note="21 copies 2 mer aa 81% conserved" complement (44030. .44549) /note="match: STS: Em:GS196 match: GSS: Em:AQ585941".
                                                                                                                     /note="L1PA5 repeat: matches 5585.
43946. 43987
                                                                                                                                                                                                                                                         /note="MIR repeat: matches 69. .122 complement (41352. .41722)
                                                                                                                                                                                                                                                                                                                            40838. .40868
/note="MIR repeat: matches 122.
40869. .41011
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="match: GSS: Em:AQ133010"
38414. .38743
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29670. .29940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="L2 repeat: matches 2299. .2432 of consensus" 27793. .29016
                                   complement (44282.
                                                                                                                                                                                                                                                                                                                                                                                              39288. .39581
                                                                                                                                                                                                                                                                                                                                                                                                                                38974. .39189
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complement(37945. .38333)
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4981. .36185
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note="MIR repeat: matches 189. .250 of consensus"
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                                                                                                                                                                                        2254. .43416
                                                                                                                                                                                                                                                                                                        note="FLAM_C repeat: matches 3. .133 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="CpG island"
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                   282. .44623)
GSS: Em:AQ776653"
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AC093533 AC011082
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Submitted (31-AUG-2001) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 154814)
DOE Joint Genome Institute and Stanford Human Genome Center.
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19; Conserv
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On or before Mar 26, 2003 this sequence version replaced
gi:6006258, gi:15383822.
Draft Sequence Produced by DOE Joint Genome Institute
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Mammalia; Eutheria; Primates; Catarrhini
1 (bases 1 to 154814)
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Estimated Total Number of Errors
Location/Qualifiers
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Submitted (26-MAR-2003) DOE Joint Genome Institute, 2800 Mitchell
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46044. .46305
/note="AluSg repeat: matches 39. .300
46439. .46658
                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
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                            161304 bp DNA clone RP11-20K23, WORKING
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100.0%; Pred. No.
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                             linear HTG 16-MAR-2000
DRAFT SEQUENCE, 19 unordered
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Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehozzky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,
Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 16, 2000 this sequence version replaced gi:6721350. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 161304)

Birren,B., Linton,L., Nusbaum,C. and Lander,E.

Homo sapiens, clone RP11-20K23

Unpublished
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                         arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                          as soon as in
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Center clone name: 20 K 23
Center clone name: 20 K 23
Center clone name: 20 K 23
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 148819 bases at least Q40
Consensus quality: 154100 bases at least Q30
Consensus quality: 156644 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 4.5 in Q20 bases; Quality coverage: 3.8 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 135000; agarose-fp
Insert size: 159504; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
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                                                  1227: contig of 1227 bp in 1327; gap of 100 bp 3446: contig of 2119 bp in 3546: gap of 100 bp 5241; gap of 100 bp 5241; contig of 2038 bp in 7279: contig of 2038 bp in 7379; gap of 100 bp 9749; contig of 2370 bp in 9849; gap of 100 bp
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of 2698
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of 2639
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63755. .78005
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41008. .51635
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                 /note="assembly_fragment"
129974. .161304
                                                      /note="assembly_fragment"
100042. .129873
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19931. .23207
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                      /note="assembly_fragment"
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|328. .3446
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78005: contig of 14251 bp ii
78105: gap of 100 bp
99941: contig of 21836 bp ii
100041: gap of 100 bp
129873: contig of 29832 bp ii
129973: gap of 100 bp
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161304: contig of 31331 bp ii
cation/Qualifiers
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TITLE
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Ml3 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information the WORMPEP database can be found at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-APR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Apr 26, 2003 this sequence version replaced gi:30024500.
                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep Repeat names beginning 'Dr' were identified by the Recon repeat discovery syst (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). F
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Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 162939)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: zfish-help@sanger.ac.uk
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                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml
is from a Zebrafish BAC library
                                                                                                                                                                                                                                                                                         further information see
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                      /clone_lib="DanioKey"
27956 c 27092 g 5
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/db_xref="taxon:7955"
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19; Conserv
                                                                                                        Submitted (23-FEB-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6. On Feb 16, 2002 this sequence version replaced gi:18308807
                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 164396)
Levy, A. and Kozlowicz, A.
The sequence of Homo sap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 164396)
Sulston,J.E. and Waterston,R.
                                                                                                                                                                                                                      Submitted (16-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                     MO 63108, USA
4 (bases 1 to 164396)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                  Submitted (24-JAN-2002) Genome University School of Medicine,
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                                                              Center: Washington University Genome Sequencing Center Center code: WUGSC
Center project name: H_NH0137J16
                               Web site: http://genome.wustl.edu/gscContact: sapiens@watson.wustl.edu
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

riom more than one subcione; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D.

FEATURES

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Actual start of this clone is at base position 1 of RP11-137J16;
actual end is at base position 164396 of RP11-137J16.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="4"
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14831. .14937
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23807. .23957
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15370. .15449
/rpt_family="MalR"
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1433. .2170"
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5. .30237
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                                                                                                                                                                                                                                                                                             AL Submitted (02-Apr-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA CB 3 (bases 1 to 176785)

EB 3 (bases 1 to 176785)

EB irren, B. Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Arachchi, H.M., Barria, N., Bastien, V., Bloom, T., Anderson, S., Arachchi, H.M., Barria, N., Bastien, V., Bloom, T., Anderson, S., Cook, A., Cooke, P., Corum, B., DeArellano, K., Collymore, A., Cook, A., Cooke, P., Corum, B., DeArellano, K., Collymore, A., Cook, S., Dooley, K., Dorris, L., Erickson, J., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Kells, C., Liu, Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Madonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Madonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., MacLean, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange, Thomann, N., Stobas, M., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wand, M., Manning, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Birren,B., Nusbaum,C. and Land
musculus, clone RP24-395F1
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus (house mouse)
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                                                                                                                              Submitted (22-FBB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Feb 22, 2003 this sequence version replaced gi:20800351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
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                                             All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                  Direct Submission
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RP24-395F1, V
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DRAFT SEQUENCE, 13 unordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as soon as it is available and be preserved.
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Sequencing vector: Plasmid, n/a, 100% of read Chemistry: Dye-terminator Big Dye; 100% of read Resembly program: Phrap; version 0.960731

Consensus quality: 173096 bases at least Q40

Consensus quality: 175223 bases at least Q30

Consensus quality: 175223 bases at least Q20

Tracery airs. 16000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Insert size: 168000; agarose-fp
Insert size: 175585; sum-of-contigs
Quality coverage: 8.9 in Q20 bases; agarose-fp
Quality coverage: 8.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L25615
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116540
154763
154863
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Center code: WIBR
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                                    /note="assembly_fragment"
91745. .92427
                                                                                                             /note="assembly_fragment"
89875. .90628
                                                                                                                                                            vector_side:left"
                                                                                                                                                                                       clone_end:SP6
                                                                          /note="assembly_fragment"
90729. .91644
                                                                                                                                                   89055.
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                                                                                                                                                                                               note="assembly_fragment
                                                                                                                                                                                                                              1. .88954
                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                               db_xref="taxon:10090"
   note="assembly_fragment"
12528. .93177
                                                                                                                                                                                                                                                                clone="RP24-395F1"
                                                                                                                                                                                                                                                                                                                                                                       116539: gap of 100 bp
154762: contig of 38223 bp in length
154862: gap of 100 bp
176785: contig of 21923 bp in length
                                                                                                                                                                                                                                                                                                 type="genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88954: contig of 88954 b
89054: gap of 100 bp
89774: contig of 720 bp
89874: gap of 100 bp
                                                                                                                                                                                                                                             lib="RPCI-24 Male Mouse BAC"
                                                                                                                                                     .89774
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contig of 683 l
gap of 100 bp
contig of 650 l
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gap of 100 bp
contig of 2157 bp in length
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                                                                                                                                                                                                                                                                             Direct Submission.

Submitted (21-MAY-2002) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-03-9170)

On Aug 21, 2002 this sequence version renlaced circumaters.
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Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
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                                                                                                                        Submitted (08-JAN-2003) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                              Submitted (07-JUN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 192409)
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Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.
Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.h NOTE: This is a "working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be preserved.
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Chemistry: Dye-terminator Big Dye: 95% of reads
Consensus quality: 171549 bases at least Q40
Consensus quality: 181986 bases at least Q30
Consensus quality: 188593 bases at least Q20
Estimated insert size: 208123; sum-of-contigs estimation
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Center project name: HBMC
Center clone name: RP11-466116
----- Summary Statistics
Sequencing vector: M13;
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Contact: hgsc-help@bcm.tmc.edu
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Center Code: BCM
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RS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

RS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,

Anderson,S., Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B.,

Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,

Choepel,Y., Colangelo,M., Gollins,S., Collymore,A., Cook,A.,

Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,

Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,

Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,

Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,

Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,

Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Liu,G.,

MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,

McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,

McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,

McCarthy,M., McEwan,P., McKernan,K., Naylor,J., Nguyen,C.,

Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D.,

Oliver,J., Fetta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,

Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P.,

Raymond,C., Severy,P., Sougnez,C., Spencer,B., Stange-Thomann,N.,

Stojanovic,N., Strauss,N., Subramanian,A., Tralamas,J., Tesfaye,S.,

Theodore,J., Topham,K., Travers,M., Travis,N., Trigillo,J.,

Voung,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission
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Submitted (20-JUL-2001) Whitehead Institute/MIT Center for Gence Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (Dases 1 to 201886)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Bloom,T., Boguslavkly,L., Boukhgalter,B., Brown,A., Camapatata,J., Campopiano,A., Chang,J., Charg.J., Char
                                                                                                                                                                                                                                                                                 Direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Cat
1 (bases 1 to 201886)
Birren,B., Linton,L., Nusbaum,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIG.
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Homo sapiens chromosome 8, clone RP11-661A3, complete sequence.
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114201
128917
129017
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/mol type="genomic DNA"
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/clone="RP11-466116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location,
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128916: contig of 14716 bp in 1
129016: gap of unknown length
146607: contig of 17591 bp in 1
146707: gap of unknown length
166333: contig of 19646 bp in 1
166453: gap of unknown length
166453: gap of unknown length
192409: contig of 25956 bp in 1
pcation/Qualifiers
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Pred. No.
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                                        Chang, J.,
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72/2/2/1/1/1/1/1/1/1/1/1/1/1/1/1/1/1/1/1	/clone="RP11-661A3" /clone=lib="RPCI-11 Human Male BAC" 4356. 4523 /rpt_family="HALlb" repeat_region /rpt_family="HALlb" repeat_region /rpt_family="AluJFRAM" repeat_region /rpt_family="AluJFRAM" repeat_region /rpt_family="AluJFRAM" repeat_region /rpt_family="(TA)n" repeat_region /rpt_family="(TA)n" repeat_region /rpt_family="L3" repeat_region /rpt_family="AluSx" repeat_region /rpt_family="RNA-Glu-GAG" repeat_region /rpt_family="RNA-Glu-GAG" repeat_region /rpt_family="RNA-Glu-GAG" /rpt_family="AluSx" repeat_region /rpt_family="AluSx" /rpt_family="AluSx" /rpt_family="AluSx"	All repeats were identified using RepeatMasker: Smit, A.E.A. & Green, P. (196-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html	Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kartasa, A., Kells, C., LaRocque, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Liu, G., MacCean, C., Macdonald, P., Major, J., Marquis, N., Marthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrin, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Milson, B., Wu, X., Wyman, D., Ye, W.J., Vong, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Submitted (06-JUN-2002) Whitehead Institute/MIT Center for Genome Submitted (06-JUN-2002) Whitehead Institute/MIT Center for Genome Comment.
repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region		repeat_region	repeat_region
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REFERENCE
AUTHORS
TITLE
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VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL REFERENCE
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ORGANISM
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AC024249/c
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TITLE
JOURNAL
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                                                                                                                                                                                                                                Center project name: H NH0661A03

Sequencing vector: Summary Statistics
Sequencing vector: M13; 100%
Sequencing vector: M13; 100%
Sequencing vector: Plasmid; 0%
Chemistry: Dye-terminator Big Dye; 8% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 192742 bases at least Q40
Consensus quality: 194956 bases at least Q40
Consensus quality: 196287 bases at least Q20
Insert size: 199083; sum-of-contigs
Quality coverage: 4.81 in Q20 bases; sum-of-contigs
Quality coverage: 4.81 in Q20 bases; sum-of-contigs
Quality coverage: 4.95 in Q20 bases; sum-of-contigs
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19; Conserv
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Waterston, R.H.
Direct Submission
Submitted (28-FEB-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Apr 21, 2000 this securi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo
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Waterston, R. H.
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AC024249.3 GI:7631100
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center
Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens chromosome
                                            NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
    be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens
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45342. .45403
/rpt_family="(TATG)n"
45409. .45463
/rpt_family="MLT2D"
complement(45464. .45891)
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complement(44323. .44921)
/rpt_family="L1"
44923. .45311
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1100: contig of 1100 bp in length
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68846. .74175
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65137. .68745
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159101: gap of unknown length
169783: contig of 10682 bp in
169883: gap of unknown length
202983: contig of 33100 bp in
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 NOTE: This is a 'working draft' sequence. It currently
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Chcepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Chcepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., Crant, G., Hagos, B., Heaford, A., Horton, L., Gardyna, S., T., Lehoczky, J., Levine, R., Lieu, C., Llu, G., Locke, K., Macdonald, P., Marquis, N., McBwan, P., McGurk, A., McKernan, K., McDheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone RP11-119P12
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                         Center project name: L5386

Center clone name: 119 P 12

Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 161318 bases at least Q40
Consensus quality: 161318 bases at least Q30
Consensus quality: 194050 bases at least Q20
Insert size: 203818; sum-of-contigs
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Quality coverage: 3.2
                                                                                                                                                                                                                                                                                                                                                                        Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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HTGS_PHASE1; HTGS_DRAFT.
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consists of 49 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contig are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="18"
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                                                                                                                                                                                Birren, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Gardyna, S., Gord, S., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kolline, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nuyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Smith, C., Spencer, B., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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HTG; HTGS PHASE2; HTGS_DRAFT; HTGS_FULLTOP
Mus musculus (house mouse)
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 24, 2002 this sequence version replaced gi:20389460. All repeats were identified using RepeatMasker:
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* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 17004: contig of 17004 bp in length

1 17005 17104: gap of 100 bp

1 17105 19927: contig of 2823 bp in length

2 19928 20027: gap of 100 bp

2 2028 82596: contig of 62669 bp in length

2 2028 82596: gap of 100 bp

3 82797 150567: gap of 100 bp

3 82797 150567: gap of 100 bp

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5 150668 216488: contig of 65821 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                        AAATTTTTGATGGCCTTAA 118180
                                                                                                                    AAATTTTTGATGGCCTTAA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 198000; agarose-fp
Insert size: 216088; sum-of-contigs
Quality coverage: 11.0 in Q20 bases; agarose-fp
Quality coverage: 10.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of read Assembly program: Phrap; version 0.960731 Consensus quality: 215495 bases at least Q30 Consensus quality: 215807 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: sequence submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center project name: L21089
Center clone name: 310_G_22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WIBR
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Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment" 150668. .216488
                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment"
82797. .150567
                                                                                                                                                                                                                                                                                                                                                                                                                                              20028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vector_side:left"
17105. .. 19927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone_end:SP6
                                                                                                                                                                                                                                                                                          /note="assembly_fragment" 39028 c 39940 g 69121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="RPCI-24 Male Mouse BAC"
1. .17004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="RP24-310G22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                .82696
                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                             Score 19;
Pred. No.
                                                                                                                                                                                          DB
23;
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                                                                                                                                                                                                                    Length 216488;
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DEFINITION

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KEYWORDS
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                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                  JOURNAL
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                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                     RS Milen, C., Marie, Metzker, M.Lee, Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalbachi, V., Avyaei, A., Avodeji, M., Baca, E., Baden, H., Balden, H., Divya, K., Davila, M., Balden, C., Coyle, M., Cree, A., D. Souza, L., Davila, M., Buger, C., Coyle, M., Cree, A., D. Souza, L., Davila, M., Balden, C., Borter, M., Foster, P., Fernandez, S., Finley, M., Flagg, M., Forbes, L., Poster, M., Foster, P., Fraser, C.M., Gabis, A., Garta, R., Garcia, A., Garrer, T., Garza, M., Garrer, M., Garcia, M., Garrer, M., Garcia, A., Garrer, T., Garza, M., Garrer, M., Garcia, M., Garci
Direct Submission
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus clone CH230-21A12, WORKING DRAFT SEQUENCE, 2
                                                                                                                        Baylor Plaza, Houston,
3 (bases 1 to 222692)
                                                                                                                                                      Submitted (29-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC123450.3 GI:25086744
                                                                                          Rat Genome Sequencing Consortium
                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                     Worley, K.C.
                                                                                                                                                                                                                                                                                                                           Unpublished
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AC127208/c
LOCUS
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VERSION
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Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:22856157.
On Nov 19, 2002 this sequence version replaced gi:22856157.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome
AC127208
AC127208.3 GI:30522796
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                    AC127208 228638 bp DN Rattus norvegicus clone CH230-160K20,
                                                                                                                 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are rouse of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                    TTTATAAAGCACTCAATTT 27
                                                                                                                                                                                                                                                                                                                                                             TTTATAAAGCACTCAATTT 77599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: GXOG
Center clone name: GXOG
Center clone name: GXOG
1------ Summary Statistics
Assembly program: Phrap; version 0.990329
Assembly program: Phrap; version 1.990329
Consensus quality: 212567 bases at least Q40
Consensus quality: 214333 bases at least Q20
Consensus quality: 215448 bases at least Q20
Estimated insert size: 217382; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="wgs_contig"
1662. .2989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="wgs_contig"
47682 c 48203 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221265: contig of 221265 bp in length 221365: gap of unknown length 222692: contig of 1327 bp in length.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                       DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bryant, N., Bunay, C., Burch, F., Burrell, K., Cardenon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z.,
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Sozal,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dihih, H., Divya, K.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dihih, H., Divya, K.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dihih, H., Divya, K.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dihih, H., Divya, K.,
Delgado, O., Denson, S., Den, A., Davbin, K., Daval, B., Eaves, K.,
Egan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flaegy, M., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guvara, W.,
Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
Harrwey, Y., Havylak, P., Haddun, S.L., Hodgson, A., Hopues, M.,
Hollins, B., Howells, S., Hulyk, S., Hume, J., Glebridd, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpathy, S., Kelly, S., Kally, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Liu, J., Liu, W., Latte, M., Mannoud, M., Malloy, K., Mangum, A.,
Manchantie, M., Martin, K., Martin, R., Martinez, E.,
Manchartis, C., Minja, E., Monremayor, J., Moore, S.,
Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Manchartis, C., Ball, M., Newton, N., Martin, R., Pal, S., Parke, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pul, L. L.,
Pul, M., Reilly, M., Reilly, M., Reilly, R., Reyes, K., Regier, M., Reigh, R.,
Reilly, B., Reilly, M., Reil
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 10, 2003 this sequence version replaced gi:23264335. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
                                                                                                                                                                                                                                                                                                                                                      Submitted (14-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Bene
Baldwin,D., Blank,D., Blankenburg,K., Blyth,P., Brown,M.,
Biswall,K., Blar,J., Blankenburg,K., Blyth,P., Brown,M.,
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                                                                                                                                                                                                                                                                              Genome Sequencing Consortium.
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l Similarity
19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.)
                                                                                                                                    66681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: GGJU
Center clone name: CH230-160K20
Center clone name: CH230-160K20
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 221580 bases at least Q40
Consensus quality: 223734 bases at least Q30
Consensus quality: 223997 bases at least Q20
Estimated insert size: 229143; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor Co
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clone_end:T7"
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clone_end:Sp6"
complement(4854. 5756)
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225364. .227242
                                                                                                                                                                                                                                                             /note="clone_boundary
clone_end:T7
site:EcoRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/mol_type="genomic DNA"
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                                                                                Submitted (23-JUL-2002) Human Genome Sequencing Center, Depay of Molecular and Human Genetics, Baylor College of Medicine, Baylor Plaza, Houston, TX 77030, USA On Jul 23, 2002 this sequence version replaced gi:6997287.
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (17-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
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Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                             of Molecular and Human
Baylor Plaza, Houston,
3 (bases 1 to 228802)
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Direct Submission
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                                                                                                                                                                                                                                                                                             Direct Submission
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Ephydroidea; Drosophilidae; Drosophila.
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                                             Jul 23, 2002 this sequence version replaced gi:6997287
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Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                          LOCUS
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                                                  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                          KEYWORDS
                                                                                                                                       VERSION
                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                  AC096231
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local
     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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163358
AC0962318
AC096231.8 GI:30522338
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
HTG; HTGS_PHASE1; (Norway rat)
                                                                                                                                                                                                                                                                                                                                             l Similarity
                                                                                                       Rattus norvegicus clone CH230-33C23, ***, 2 unordered pieces.
                                                                                                                                                     AC096231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.)

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 9 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                               ATTTTCTACCCGGGCTCAC 163340
                                                                                                                                                                                                                                                                                                 ATTTTCTACCCGGGCTCAC 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  64009 a 50361 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: Phrap; version 0.990329 Consensus quality: 254374 bases at least Q40 Consensus quality: 25831 bases at least Q30 Consensus quality: 271567 bases at least Q20 Estimated insert size: 222216; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: Plasmid;
Sequencing vector: M13;
Chemistry: Dye-terminator Big Dye: 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: DRJG
Center clone name: RP98-46E23
Center clone name: RP98-46E23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: hgsc-help@bcm.tmc.edu
----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17230
17330
20216
20316
20316
33624
33724
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14409
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9774
12081
12181
                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="RP98-46E23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20215: contig of 2886 bp in length
20315: gap of unknown length
33623: contig of 13308 bp in length
33723: gap of unknown length
47696: contig of 13973 bp in length
47796: gap of unknown length
95023: contig of 47227 bp in length
95123: gap of unknown length
228802: contig of 133679 bp in length
                                                                                                                                                                                                                                                                                                                                    100.0%; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9773:
12080:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14408: gap of unknown length
17229: contig of 2821 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14308:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9673: contig of 9673 bp in length
9773: gap of unknown length
2080: contig of 2307 bp in length
                                                                                                                                                                                                                                                                                                                                                                                      8.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              49400 g 64230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of contig
                                                                                                                                                                                                                                                                                                                                          Score 19; DB; Pred. No. 23; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of unknown len
contig of 2128 bp
gap of unknown len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown length
                                                                                                                                                     đđ
                                                                                                                                                                                                                                                                                                                                                                DB
23;
                                                                                                                           DNA 1111Ca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in length
                                                                                                                                                                                                                                                                                                                                                                                      Length 228802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  802 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 draft_data.html).
                                                                                                                                   IN PROGRESS
                                                                                                                                                     HTG 10-MAY-2003
                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                             0
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REFERENCE

AUTHORS

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Cardenas, V., Carter, K., Chen, G., Chen, E., Chen, E., Chen, C., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, I., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, I., Delgado, O., Denson, S., Deramo, C., Dingy, Dinh, H., Divya, K., Delgado, O., Denson, S., Deramo, C., Dingy, Dinh, H., Divya, K., Deparer, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Bscotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, M., Forbes, I., Foster, M., Foster, P., Fan, G., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Gebregoorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gunarathe, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Hernandez, J., Harvey, Y., Havlak, P., Haddun, S. I., Holgson, A., Hornes, J., Johnson, B., Johnson, R., Johnson, A., Juckson, A., Juckson, A., Hander, S., L., Holgson, A., Hongues, M., Hernandez, J., Liu, Y., London, P., Longotre, S., Lopez, J., Liu, Y., London, P., Longotre, S., Lopez, J., Liu, Y., London, P., Longotre, S., Lopez, J., Lowis, L., Liu, Z., Liu, J., Liu, Y., London, P., Longotre, S., Lopez, J., Lowester, M., Martin, K., Martin, R., Martinez, E., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Martinez, E., Martinez, E., Martinez, E., Morris, S., Munidasa, M., Murphy, M., Naris, S., Naris, S., Nuncer, G., Minja, E., Kontens, S., Patks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Sanders, M., Sodergre, S., Scott, G., Shatsman, S., Sheen, H., Shetty, J., Shoratbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sned, A., Sodergre, S., Scott, G., Shatsman, S., Sheen, H., Shetty, J., Watter, C., Shatsman, S., Sheen, H., Shetty, J., Watter, K., Watter, F., Wang, J., Watter, K., Watter, C., Shatsman, S., Sheen, H., Shen, J., Watter, S., Watter, F., 
                                                                                                                                            Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:25013165.
The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, K., Blyth, P., Brown, M., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.
and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                      Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 229077)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams, C., Alder, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 40
AC095567/c
                                                                                                                REFERENCE
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ORIGIN
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                                                                                                                                                                                                                                                                                                                 SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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                                                                                AUTHORS
                                                                                                                                                                                                                                                                         ORGANISM
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REFERENCE AUTHORS TITLE

JOURNAL

TITLE JOURNAL

REFERENCE

AUTHORS

JOURNAL

COMMENT

Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, (Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Bad

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;

Adams, C., Alder, J.,

Mammalia; Eutheria;

Rattus.

(bases 1 to 229140)

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                              88115
                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
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Rattus norvegicus (Norway Rattus norvegicus
                                                    HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
                                                                                  AC095567.6 GI:30467314
                                                                                                                                                                 Rattus norvegicus clone CH230-7016, ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.)
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                         TACTCAGAAATTTTTGATG 47
                                                                                                                                            unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64800 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will be preserved.
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Center clone name: CH210-33C23
Center clone name: CH220-33C23
Center clone name: CH220-33C23
Center Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 212493 bases at least Q40.
Consensus quality: 215756 bases at least Q30
Consensus quality: 217525 bases at least Q20
Estimated insert size: 229406; sum-of-contigs estimation
Quality coverage: 6x in.Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           225593
225693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="wgs_contig"
42460 c 40825 g 70150 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 225592: contig of 225592 bp in length
3 225692: gap of unknown length
3 229077: contig of 3385 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="CH230-33C23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .229077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 19;
Pred. No.
                                                                                                                                                                                              229140 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10842 others
                                                                                                                                                                       SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 229077;
                                                                                                                                                                                                       linear
                                                                                                                                                                       IN PROGRESS ***
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Claveland, C., Cockrell, R., CARN, K., CREN, K., CREN, E., CREN, E., CHEN, C., COYLÉ, M., Cree, A., D'SOUZAL, Davila, M.L., Davis, C., Davy-Carroll, D. De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Drager, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Engere, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Filley, M., Flagg, N., Forbes, L., Foster, M., Garex, M., Gebregeorgia, E., Geer, K., Gill, R., Gracia, A., Garner, T., Garza, M., Gebregeorgia, E., Geer, K., Gill, R., Gracia, A., Garner, T., Garza, M., Gebregeorgia, E., Geer, K., Gill, R., Gracia, A., Garner, T., Garza, M., Gebregeorgia, E., Geer, K., Gill, R., Gracia, A., Henderson, N., Hernandez, J., Hernandez, J., Harvey, Y., Havlak, P., Haddin, S. L., Hedgson, A., Hogues, M., Hernandez, J., Houllins, B., Howells, S., Hallyk, S., Hame, J., Idlebird, D., Jackson, A., Jokeson, A., Jokeson, A., Houllins, B., Howells, S., Hallyk, S., Khan, Z., King, L., Kovar, C., Kowis, C., K., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Lovan, J., Lewis, L., Liz, T. Liu, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, M., Malloy, K., Mangum, A., Mangum, A., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, S., Mchell, T. Z., Meenen, E., Mawhiney, S., McLeod, M., P., Martin, R., Martin, R., Martinez, B., Mawhiney, S., McLeod, M., Malloy, K., Mangum, A., Mangum, S., Munghy, M., Norris, S., Munidasa, M., Norris, S., Nuris, S., Nu
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 9, 2003 this sequence version replaced gi:24940786. The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 229140)
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contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                               and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separate by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
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                                                                           Rattus norvegicus clone CH230-318P21,
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* Consists of 7 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: hgsc-help@bcm.tmc.edu
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226284: gap of unknown len
229140: contig of 2856 bp
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100.0%; Pred. No.
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On Nov 19, 2002 this sequence version replaced gi:23194968. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
                                                                                                                                                                                                                                                                                                                                           Submitted (05-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                           Submitted (19-NOV-2002) Human Genome Sequencing Center, Depa of Molecular and Human Genetics, Baylor College of Medicine,
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently

consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary, Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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------ Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 209814 bases at least Q40
Consensus quality: 211069 bases at least Q20
Consensus quality: 211069 bases at least Q20
Consensus quality: 211999 bases at least Q20
Estimated insert size: 220261; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:
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235182 bp
clone CH230-11L9,
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                                                                                                                                                                                                                                                                                                 Score 19;
Pred. No.
                                                                                                                                                                                                                                                                           Mismatches
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  DNA linear WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                        20652 others
                                                                                                                                                                                                                                                                                                                          Length 233163;
                                 HTG 10-MAY-2003
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AC099082.5 GI:30522836 HTG; HTGS_PHASE1; HTGS_

HTGS_DRAFT; HTGS_FULLTOP (Norway rat)

AC099082

unordered pieces.

SEQUENCE

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TITLE
JOURNAL
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AUTHORS
TITLE
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, J., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutcon, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, M., Weight, N., Wilson, R., Wleczyk, R., Wooden, H., Worley, K., Williams, G., Wilson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 10, 2003 this sequence version replaced gi:23096197. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (09-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 235182)
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Anyalebechi,V., Aoyagi,A., Avodeii.M
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Rodentia;
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                              ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          101737
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COMMENT

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assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
Rattus norvegicus clone CH230-31B17, ***, 9 unordered pieces. AC12629B
                                                                                                                                                                                                                                                                                                                                                              . Similarity
19; Conser
                                                                                      AC126298
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NOTE: This is a 'working draft' sequence. It currently consists of 7 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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228692
228792
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232014
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223577
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226007
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39463 c 41351 g 63457 t
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="CH230-11L9"
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223576: gap of unknown length
224676: contig of 1100 bp in length
224776: gap of unknown length
225906: contig of 1130 bp in length
225906: gap of unknown length
225906: gap of unknown length
227139: contig of 1133 bp in length
227239: gap of unknown length
228691: contig of 11452 bp in length
2286791: gap of unknown length
231913: contig of 3122 bp in length
231913: gap of unknown length
231913: contig of 3120 bp in length
231913: contig of 3169 bp in length
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                                                                                      235700 bp
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23;
                                           DNA
7. *** SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23647 others
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                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Allen, C., Allen, H., Albirooks, S., Amin, A., Augulano, D., Anyalebechi, V., Aoyaqi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranika, D., Barber, M., Barnisead, M., Benhmed, F., Baldwin, D., Bandaranika, D., Barber, M., Barnisead, M., Benhmed, F., Blaiwalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Chan, J., Charez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Charez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Charez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Charber, M., Bulay, C., Burch, P., Burrell, K., Calderon, E., Deugand, C., Coyle, M., Cree, A., D'Souza, L., Davila, G., Davy-Carcoll, L., De Man, Y., Chen, Z., Chu, J., Charber, M., Chen, S., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Charber, M., Chen, S., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chen, S., Chen, S., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chen, S., Chen, S., Chen, G., Chen, R., Chen, Y., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, S., Chen, S., Chen, S., Chen, S., Chen, S., Chen, C., Chen, J., Chen, J
                                                                                                                                                                                                                                       Submitted (05-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235700)
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 19, 2002 this sequence version replaced gi:21702798. The sequence in this assembly is a combination of BAC based reads
                                                                                                      Direct Submission
Direct Submission
Submitted (22-SEP-2002) Human Genome Sequencing
Submitted (22-SEP-2002) Human Genetics, Baylor College
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                                                                                                                                                                                                                                                                                                                                                                                                       Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                        Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                            Center, Depa
of Medicine,
                                                                                                                                              Department
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Consensus quality: 161627 bases at least Q40
Consensus quality: 168027 bases at least Q30
Consensus quality: 172221 bases at least Q30
Consensus quality: 172221 bases at least Q30
Consensus quality: 172221 bases at least Q20
Estimated insert size: 192265; sum-of-contigs estimation
Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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121152. .121400
/note="clone boundary
clone_end:T7
                                                                                                                                                                                                                                           /note="wgs_contig"
42447. .43559
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56213. .57746
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121152. .121288
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30002. .31205
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103185. .104507
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                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Rattus norvegicus"

mol_type="genomic DNA"
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226484: gap of unknown length
228083: contig of 1599 bp in length
228183: gap of unknown length
229228: contig of 1045 bp in length
229328: gap of unknown length
230723: contig of 1395 bp in length
230723: contig of 1395 bp in length
230723: gap of unknown length
23136: gap of unknown length
23136: gap of unknown length
233236: gap of unknown length
235700: contig of 2464 bp in length
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220901. .222607 /note="wgs_end_extensior clone_end:T7"

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REFERENCE
AUTHORS
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RS Muzzy, Narie., Merzker, Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alebrooks, S., Amin, A., Angulano, D., Allen, C., Allen, H., Alebrooks, S., Amin, A., Angulano, D., Allen, C., Allen, H., Alebrooks, S., Amin, A., Angulano, D., Allen, C., Allen, H., Alebrooks, S., Amin, A., Angulano, D., Alebrooks, S., Amin, A., Angulano, D., Alebrooks, S., Amin, A., Angulano, D., Alebrooks, S., Paren, M., Barnstead, M., Berande, F., Brands, C., Cocker, S., Chen, S., Chen, Y., Chen, Z., Chen, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Dery-Carroll, L., De Anda, C., Dederich, D., Davila, M. L., Davis, C., Dary-Carroll, L., De Anda, C., Dederich, D., Dederich, D., Davila, M. L., Davis, C., Denn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Bugene, C., C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Derboon, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Bugene, C., Evans, C.A., Falls, T., Fan, G., France, F., Haland, S., Dunn, A., Gardy, M., Guerra, W., Guevara, W., Gubregoorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Guevara, W., Gubred, S., Haladin, S., Henderson, N., Hernandez, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Loulseged, H., Loulseged, H., Loulseged, H., Johnson, B., Johnson, R., Jolivet, A., Karyathy, S., Kelly, S., Kaly, S., Khan, Z., Kan, J., Kowar, C., Kwais, C., Kraft, C.L., Lebow, H., Lewan, J., Lewis, L., Lid, Z., Liu, J., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Louss, L., Lid, Z., Liu, J., Liu
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AUTHORS
TITLE
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Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 13, 2003 this sequence version replaced gi:23111081. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley, K.C.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center code: EDM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
clone_end:T7"
1550. .2265
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clone_end:T7
site:EcoRI
                                                                                                                                                                /note="wgs_end_extension
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                                                                                                                                                                                                                                                                                                                   organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                     clone="CH230-106J14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     .242803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238212: contig of 238212 bp in length 238312: gap of unknown length 241662: contig of 3350 bp in length 241762: gap of unknown length 242803: contig of 1041 bp in length.

    Genome Center

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REFERENCE
AUTHORS
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AC097237/c
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
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RS Muzny, D. Marie. Metzker, M.Lee., Abramzon, S., Adams, C., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyaliabechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chen, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Doavis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Derger, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Eggan, A., Escotto, M., Eugene, C., Bans, C.A., Falls, T., Fan, G., Farser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garrer, T., Garza, M., Gebregoorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, A., Hines, S., Haddun, S.L., Hodgson, A., Hogues, M., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, M., Jackson, L., Johnson, B., Johnson, R., Johnson, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21572 TTATAAAGCACTCAATTTC 21590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 TTATAAAGCACTCAATTTC 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC097237 245082 bp DNA linear Rattus norvegicus clone CH230-63H19, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC097237.6 GI:30522413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67043 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 245082)
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clone_end:Sp6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _boundary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23403 others
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AL Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:22855496.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contigs caffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regler, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rockey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shenty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Snedty, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sons, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Vallas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Warren, R., Wei, X., White, F., Wang, G., Wallson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Miederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (13-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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Rat Genome Sequencing Consortium.
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Center project name: GGSB
Center clone name: CH230-63H19
Center clone name: CH230-63H19
Center clone name: CH230-63H19
Center Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 233500 bases at least Q40
Consensus quality: 236413 bases at least Q30
Consensus quality: 23644 bases at least Q30
Consensus quality: 23864 bases at least Q20
Estimated insert size: 244959; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Baylor College of Medicine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Project Information
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TITLE JOURNAL REFERENCE

TITLE JOURNAL

AUTHORS

REFERENCE

COMMENT

JOURNAL AUTHORS

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 245082: contig of 245082 bp in length. Location/Qualifiers

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.)

NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

data.html).

FEATURES

source

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/clone="CH230-63H19"
misc_feature 1..1631
/note="wgs_contig"
BASE COUNT 64097 a 51810 c 53142 g 70982 t 5051 others
ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 19; TTTATAAAGCACTCAATTT 27
Qy 9 TTTATAAAGCACTCAATTT 233550
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Search completed: February 4, 2004, 15:24:52 Job time : 3158 secs

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Minimum
Maximum
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0 seq length: 2000000000
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228
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Copyright (c) 1993 - 2004 Compugen Ltd
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2137.055 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Novel human transp	ABX61876	25	601	7.5	17	8	
Drosophila melanog	ABL22535	23	580	7.5	17	7	
Human cancer relat	ABN60692	24	564	7.5	17	on	
Human prostate exp	ABV36501	23	360	7.5	17	IJ	ი
DNA encoding novel	AAS83274	23	3414	7.9	18	4	a
Human differential	AAF30666	22	506	7.9	18	щ	Ω
Prostate cancer an	AAF30668	22	(20)	8.8	20	N	ი
Human differential	AAF30666	22	506	100.0	228	1	
Description		. B	Query Match Length DB ID		Score	Result No.	Res

05-APR-2001.

Human Oestrogen re	AAS43104	22	325791	7.5	17	5		
Human breast cance	ABT10147	24	185035	7.5	17	44		
Human cDNA differe	ABK83575	24	136284	•	17	43	Ω	
Genomic DNA encodi	ABX61804	25	40645	•	17	42		
Drosophila melanog	ABL18664	23	30143	7.5	17	41	ი	
cDNA encoding nove	ABX59821	25	29228	•	17	40	a	
Human musculoskele	AAL36833	22	29228	7.5	17	39	ი	
cDNA encoding nove	ABX59817	25	28313	7.5	17	3 8 8	ი	
Human musculoskele	AAL36829	22	28313	7.5	17	37	ი	
Streptococcus pneu	AAV52155	19	28171	7.5	17	36		
Human immune/haema	AAK84864	22	23533		17	35		
Human immune/haema	AAK84865	22	23527	7.5	17	34		
Human immune/haema	AAK84863	22	23527	7.5	17	u u		
Human novel protei	AAD16643	22	18657	7.5	17	32		
	ABL22058	23	7993	7.5	17	31	a	
Drosophila melanog	ABL14618	23	6829	٠	17	30		
	AAL04434	22	6352	٠	17	29		
DNA encoding novel	AAS30407	22	6352		. 17	28		
	ABL22059	23	5790	7.5	17	27		
	ABL22534	23	2662	7.5	17	26		
	AAK51573	22	2661		17	25		
Human polynucleoti	AAK52557	22	2652		17	24		
Human polynucleoti	AAI59024	22	2318		17	23		
Human polynucleoti	AAI60810	22	2309		17	22		
Pain regulated cDN	ABL88432	24	2279	7.5	17	21		
Nucleotide sequenc	AAA75733	21	2279		17	20		
Catalase gene of h	AAX08433	20	2264		17	19		
Streptococcus poly	ABN69051	24	2070		17	18		
Human zinc finger	ABV77738	24	1842		17	17	ი	
Arabidopsis thalia	AAC51976	21	1675		17	16		
man delta-5-	AAD31177	24	1357	7.5	17	15		
	662	25	1260	•	17	14		
Streptococcus pneu	AAV37398	19	1252	•	17	13		
O	AAS53792	23	927		17	12	ი	
	AAH04021	22	793	7.5	17	H		
neurob	45	22	773	7.5	17	10	ი	
Novel human transp	ABX61877	25	601	7.5	17	9		

ALIGNMENTS

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RESULT 1
AAF30666
ID AAF3
XX AAF3
AC AAF3
XX PCAA
DT 11-J
XX PCAA
XX PCAA
XX Homo
XX Homo
XX Homo
XX Homo
XX Homo
XX EY
FT exon
FT exon
FT exon
FT exon
FT exon
FT exon
FT W18c
FT exon
FT W020
PN W020
PD 05-A
                                                                            exon
                                                                                                                                                                                                                                                                        11-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                               AAF30666;
                                                                                                                                                                                                                                                                                                                      AAF30666 standard; cDNA; 506 BP.
                                                                                                                                               exon
                                                                                                                                                                                                    PCA3; prostate cancer; antigen; benign prostatic hyperplasia; differential expression; diagnosis; gene therapy; chromosome human; ss.
                                                                                                                                                                                                                                                 Human differentially expressed PCA3 cDNA (long form).
                                                                                                             misc_RNA
                                  WO200123550-A2.
                                                                                                                                                                                Homo sapiens
                                                                                                              /number=
27..254
                                                       /*tag= c
/number= "
                                                                                       /*tag= b
/note= "228
                                                                                                                                                         Location/Qualifiers
                                                                            255..506
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                                                                                        insertion"
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ARESULT 2
AAF30668/c
ID AAF306
XX AAF306
XX AAF306
XX II-JUN
XX Prosta
XX PCA3;
XW diagno
XX PCA3;
XW diagno
XX WO2001
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            additional 228 bp sequence, inserted between exons 3 and 4a. A 2nd camplified fragment (see AAF30667) lacks this additional sequence. The additional sequence interrupts the open reading frame of PCA3 reprotein, thereby yielding a truncated PCA3 protein. The shorter form PCA3 RNA is associated with prostate cancer whereas the longer such as benign prostatic hyperplasia. Based on the differential expression of these 2 PCA3 RNA species, protocols for the diagnosis of prostate disease are provided, including a method of diagnosing the presence or predisposition to develop prostate cancer in a patient. Also provided are therapeutic methods that use a nucleic acid encoding a differentially expressed PCA3 mRNA, or an antibody raised against such a protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acid encoding differentially expressed prostate cancer antigen 3 mRNA containing additional sequence giving rise to long PCA3 mRNA, useful for diagnosis of mammal afflicted with prostate cancer -
                                                                                    PCA3; prostate cance diagnosis; therapy;
                                                                                                                                        Prostate cancer antigen 3 (PSA3) nucleic acid.
                                                                                                                                                                                                              AAF30668;
                                                                                                                                                                                                                                             AAF30668 standard; cDNA; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human prostate cancer antigen additional 228 bp sequence, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3(a); Fig 3; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-258132/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Busse U, Chypre C,
                   WO200123550-A2
                                                                                                                                                                          11-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 506 BP; 132 A; 123 C; 108 G; 143 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-SEP-2000; 2000WO-CA01154.
                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                      147
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                                                                                                                                                                                                                                                                                                                                                         TACCCGGGCTCACCTCCGTCCCTCCATATTTGTCCTCCACTTTCACAG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTACTCGTTTCTATCCTTCCTACTCACTGTCCTCCCGGAATCCACTACCGATTTTCTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTAAGTGCTTTATAAAGCACTCAATTTCTACTCAGAAATTTTTTGATGGCCTTAAGTTCCT 60
                                                                                                                                                                                                                                                                                                                                                                                                      TCTTGCCTCGTATTGTCTGACTGGCTCACTTGGATTTATCCTCACGGAGTCTGGATTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTTGCCTCGTATTGTCTGACTGGCTCACTTGGATTTATCCTCACGGAGTCTGGATTTTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTACTCGTTTCTATCCTTCCTACTCACTGTCCTCCCGGAATCCACTACCGATTTTCTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTAAGTGCTTTATAAAGCACTCAATTTCTACTCAGAAATTTTTGATGGCCTTAAGTTCCT
                                                                                                                                                                                                                                                                                                                                   TACCCGGGCTCACCTCCGTCCCATATTTGTCCTCCACTTTCACAG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence is that of an RT-PCR-amplified fragment stee cancer antigen 3 (PCA3) mRNA that includes an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                          (first entry
                                                                                  cancer; antigen;
rapy; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 228; DB 22;
Pred. No. 4.8e-108;
                                                                                                      marker; differential expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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ARBSULT 3
AAF3066/c
ID AAF306
XX AAF306
XX AAF306
XX II-JUN
XX PCA3,
KW PCA3,
KW PCA3,
KW human,
XX
FH Key
FH Key
FT exon
FT misc_R
FT misc_R
FT exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence comprises nucleotides from human prostate cancer antigen 3 (PCA3) long mRNA (see AAF30666). Claimed isolated nucleic acid molecules consist of 10-50 nucleotides which specifically hybridise to a differentially expressed long PCA3 mRNA, and are complementary to, or consist of, at least 10 consecutive nucleotides of the present sequence. Long PCA3 mRNA, and are complementary to, or consist of, at least 10 includes a 228 bp sequence, inserted between exons 3a and 4, which is absent in short PCA3 mRNA. Short PCA3 mRNA is associated with prostate cancer. Long PCA3 mRNA is associated with a non-mallignant prostate cancer. Nan is associated with a non-mallignant prostate cancer in a patient. Also provided are therapeutic methods that use a nucleic acid encoding a therapeutic methods that use a nucleic acid encoding a differentially expressed PCA3 mRNA, or an antibody raised against such a protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                       11-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20 BP; 9 A; 1 C; 8 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid encoding differentially expressed prostate cancer antigen 3 mRNA containing additional sequence giving rise to long PCA mRNA, useful for diagnosis of mammal afflicted with prostate cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Busse U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-SEP-2000; 2000WO-CA01154.
                                                                        misc_RNA
                                                                                                                                                                                                                                                      Human differentially expressed PCA3 cDNA (long form)
                                                                                                                                                                                                                                                                                                                                              AAF30666 standard; cDNA; 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2001
                                                                                                                                                                Homo sapiens
                                                                                                                                                                                               differential expression; diagnosis; gene therapy; chromosome
human; ss.
                                                                                                                                                                                                                         PCA3; prostate cancer; antigen; benign prostatic hyperplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DIAG-) DIAGNOCURE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Page 57; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20;
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                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                      /number= "3"
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                             /*tag= b
/note= "228 bp insertion"
255..506
                                                                                                                                    Location/Qualifiers
                                                                                                       *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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ص
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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/number= "4a"

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RESULT 4
AAS833274/c
ID AAS832
XX AAS832
XX AAS832
XX DNA en
XX DNA en
XX Human;
KW food s
XX Homo s
XX HO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                             Human; chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #19078.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS83274 standard; cDNA; 3414 BP
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                               31-MAR-2000;
23-AUG-2000;
                                                                                                                       30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                            WO200175067-A2
                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of an RT-PCR-amplified fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-SEP-2000; 2000WO-CA01154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTGCTTTATAAAGCACT 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           506 BP; 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chypre C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGTGCTTTATAAAGCACT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or an antibody raised against such a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                               2000US-0540217
2000US-0649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0156594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; 123 C; 108 G; 143 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fradet Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22; Length 506; 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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RESULT 5
ABV36501/c
ID ABV36501;
XX ABV36501;
AC ABV36501;
XX Id-SEP-200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC for identifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity amino acid sequences. AAS64197-AAS94564 represent movel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed CC and to produce data for this patent did not appear in the printed CC and the print of the contained and electronic format directly from WIPO CC and the print (Ann.) And are responsed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3414 BP; 915 A; 806 C; 940 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-SEP-2002
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                                                                                          17-FEB-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human prostate expression marker cDNA 36492.
                             25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                  23-AUG-2001.
                                                                                                                                                                                                                                                                                                            WO200160860-A2
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                                                                                                                                                                                    20-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATAAAGCACTCAATTTCT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; cDNA; 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAAAGCACTCAATTTCT 1964
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                                                                                          2000US-183319P.
2000US-189862P.
                                                                                                                                                                                    2001WO-US05171.
                         2000US-207454P.
2000US-211314P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               753 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
20
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13-DEC-2000;

2000US-255281P

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RRSULT 6
ABN60808
ID ABN6
XX ABN66
XX ABN66
XX ABN66
XX Huma
XX Huma
XX Huma
XX Homc
XX Gene
XX Gene
XX Homc
X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                              Escobedo
Lamson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cancer related polynucleotide SEQ ID NO 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 360
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                                                         WPI; 2002-241905/29
                                                                                                                                                                                               (CHIR )
(HYSE-)
                                                                                                                                                                                                                                                                                16-AUG-2000; 2000US-226326P
                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
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                                                                                                                                                                                                                                                                                                                                       16-AUG-2001; 2001WO-US25840
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200214500-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient, assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; gene expression;
herapy; cancer; tumour; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                               CHIRON CORP.
HYSEQ INC.
                                                                                                              J, Garcia
, Scott EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGATTTTCTATTTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGATTTTCTATTTCTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP; 104
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                                                                                      A PD, Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry
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                                                                                                              Sudduth-Klinger J, Reinhard C,
ang G, Kassam A, Pot D, Labat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Monahan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 17;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene mapping; tissue profiling;
ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for inhibiting prostate cancer
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                                                                                                                                           Randazzo
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New nucleic acid for producing a polypeptide,

detecting differentially

sequence data

for this patent did not

form part of the

printed

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ARESULT 7
ABLIZE 11
ABLIZE 12
AC ABLIZ
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                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01950-ABL16175) and the encoded proteins (ABL5737-ABB72072).
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        CC transporter subfamily. (I) and the nucleic acid encoding it (II) can be considered to the identification of therapeutic proteins and serve as targets, aid in the identification of therapeutic proteins and serve as targets for the certainty. (I) is used to raise antibodies or to elicit another immune cresponse, as a reagent in biological fluids, and as markers for tissues in which the corresponding protein is preferentially expressed. The creament of the proteins isolated from humans and their human/mammalian conthologues serve as targets for identifying agents for use in mammalian conthologues serve as targets for identifying agents for use in mammalian conthologues serve as targets for identifying agents for use in mammalian conthologues serve as targets for identifying agents for use in mammalian conthologues serve as targets for identifying agents for use in mammalian conthologues serve as targets for identifying agents for use in mammalian conthologues serve as targets for identifying agents for use in mammalian conthologues are related to members of the GABA neurotransmitter contains on the protein and peptides also provide a target continuous and are useful for treating a disorder characterised by the continuous are also useful for assession of the protein. The contains are also useful for assession of the protein. The contains are considered and aberrant subcellular contains and contains and aberrant subcellular in various triceriae in a considered and assert and and aberrant subcellular contains and and are useful as in various triceriae in a considered and assert and and assert and and aberrant subcellular contains and and assert a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human transporter protein,
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                                                                                                                                                                                                                                                                                                                                                        is related to the gamma-aminobutyric acid
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17; Conserv
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        The invention describes an isolated human transporter peptide (I) that is related to the gamma-aminobutyric acid (GABA) neurotransmitter transporter subfamily. (I) and the nucleic acid encoding it (II) can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the development of human therapeutic agents that modulate transporter activity. (I) is used to raise antibodies or to elicit another immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, and as markers for tissues in which the corresponding protein is preferentially expressed. The transporter proteins isolated from humans and their human/mammalian orthologues serve as targets for identifying agents for use in mammalian therapeutic applications, and biological assays related to transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmacogenomic analysis, for tissue typing and for inhibiting protein function. (II) is useful for constructing recombinant vectors, host cell and transgenic animals, for designing ribozymes; in drug screening; in diagnostic assays for qualitative changes in gene expression, particularly in qualitative changes that lead to pathology; in gene therapy; and to detect mutations in genes encoding transporters. This sequence represents a polynucleotide related to the novel human aminobutyric acid (GABA) transporter related protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                          Gong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human transporter protein related polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABX61877
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                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                            Novel human transporter protein, related to gamma-aminobutyric acid neurotransmitter transporter subfamily useful as model for developin
                                                                                                                                                                                                                                                                                                                                             WPI; 2003-102517/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2002142381-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transgenic animal; ribozyme design; drug screening; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABX61877;
                                                                                                                                                                                                                                                                                                                                                                                                                          (KETC/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2001; 2001US-0818656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-MAR-2001; 2001US-0818656.
                                                                                                                                                                                                                                                                           human therapeutic targets and serves as target
                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GONG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma-aminobutyric acid; GABA; neurotransmitter transporter;
                                                                                                                                                                                                                                                                                                                                                                                                         KETCHUM K A.
DI FRANCESCO
BEASLEY E M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GONG F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTCTATTTCTTGCCTC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      601 BP; 149
                                                                                                                                                                                                                                                                                                                                                                            Ketchum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTCTATTTCTTGCCTC 110
                                                                                                                                                                                                                                             Page 76-77; 114pp; English.
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Pred. No.
   members
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G; 203 T; 1 other;
   of the GABA
                                                                                                                                                                                                                                                                                                                                                                            Beasley EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                           is model for developing for human therapeutics
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   neurotransmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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RESULT 10
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                  The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy susceptibility indicators or tumour markers for anti-cancer agents. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids originating in gene expressed in human neuroblastoma, useful as probe or primer in diagnosing prognosis of human neuroblastoma, malignancy and susceptibility indicator or tumour marker neuroblastoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAR-2000; 2000JP-0159195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2001; 2001WO-JP01629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human neuroblastoma expressed polynucleotide SEQ ID NO 661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 601 BP; 142 A; 151 C; 108 G; 199 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200166719-A1
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                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 525; 2979pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CHIB-)
                                                                                                              information for diagnosing prognosis is related to factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTCTATTTCTTGCCTC 55
                                                                                   N-myc
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100.0%;
                                                                                   TrkA
                                                                               genes.
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Pred.
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BB
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Query Match Best Local Similarity

7.5%;

Score 17; Pred. No.

68 BG

Query Match

Sequence

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232

A; 119

c;

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Score 17; 157

Sequence

773

250 A; 150 C; 120 G; 224 T; 29 other;

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                                                                                                                                              sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs asily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises at least 15 nucleotides; or the complementary strand of a polynucleotide which comprises a 5-end
                                                            AAB95893 represent human amino acid sequences; and AAH13629 represent oligonucleotides, all of which are used in the exof the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH04021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNAs -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROM; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saito K,
C, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                 ;29 to AAH13632
exemplification
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Pred. No.

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                   The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC genes themselves and the encoded proteins. The prokaryotes used are CC invention is also useful for the identification of potential new targets CC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used CC identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen CC for homologous nucleic acids which are required for cell proliferation in CC a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part CC format directly from WIPO at CC format directly from WIPO at CC format directly from WIPO at
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AAS53792/c
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23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                  New polynucleotides for the identification antibiotics, comprise sequences of antisens
Sequence 927
                                                                                                                                                                                                                                                                                                                       Claim 27; Seq ID No 7429; 511pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAR-2001; 2001WO-US09180.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ds; prokaryotic
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2000US-206848P.
2000US-207727P.
2000US-242578P.
2000US-25362SP.
2000US-257931P.
2001US-269308P.
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 ВP;
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Xu HH;
314 A; 176 C; 196 G; 241 T; 0 other;
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Query Match

7.5%;

Score 17;

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Length 927;

Matches

Conservative

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RESULT 13
AAV37398
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                                                               S. pneumoniae. Its encoded protein, or agonists of it, to may be useful as an antibacterial for treatment or prevention of infection, specifically caused by S. pneumoniae (particularly meningitis) but possibly also Helicobacter (pylori (ulcers and gastric cancer). It may be off particular (use before insertion of an in-dwelling device or any other invasive procedure. The protein, or nucleic acid encoding it, can also be used in vaccines to induce a cellular and/or humoral immune response, or to screen for other antibacterials. The DNA may also contain flanking sequences that are potential sources of control elements for bacterial can be used diagnostically, e.g. to detect a mutation for servotyping or classifying infectious agents.
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          Query Match
Best Local
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                                             Sequence
                                                                                                                                                                                                                                                                                                    e.g. for identifying
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                                                                                                                                                                                                                                          The sequence is that of a coding region isolated from
                                                                                                                                                                                                                                                                  Claim 1; Page 104-105; 130pp; English
                                                                                                                                                                                                                                                                                                                  New isolated nucleic
                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAW61010.
                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-286586/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9819689-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       coding region;
infection; pre
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Local Similarity hes 17; Conserv
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                                             1252
                                                                                                                                                                                                                                                                                                                                                                             Hodgson JE,
Zarfos PN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prevention; meningitis; ss.
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                                             BP; 351 A; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORF; open reading frame; antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US19226
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1030..1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= putative gamma-glutamyl phosphate reductase
          100.0%;
                                                                                                                                                                                                                                                                                                    acids from Streptococcus pneumoniae anti-bacterial(s) for treatment and
                        7.5%;
                                                                                                                                                                                                                                                                                                                                                                                         Knowles DJC,
                                                                                                                                                                                                                                                                                                                                                                                                                              CORP.
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          Score 17; DB 19;
Pred. No. 68;
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                                             331 G;
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                     Length 1252;
                                             other;
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                                                                                                                                                                                                                                                                                                     prevention
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The invention relates to a protein comprising or having at least 50% clidentity to any of the 2469 amino acid sequences, identified in the especification (available on a computer readable format), or its fragment, cc expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as CC ABS56454. Also included are an antibody which binds one of the CC proteins, treating a patient by administering the protein, DNA or CC which are the nucleic acid cited above or fragments between nucleotides traget sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound to the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, sepsis, otilis media or ear infection. They are also useful in developing vaccines, diagnostics and antibotics. The methods are useful for cidentifying immunodominant proteins. The present sequence is one of contacting or preventing the proteins of the genomic sequence.
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                  the 2489 identified coding region from the genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; SEQ ID No 1819;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-040579/03
P-PSDB; ABU01335.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae type 4 strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAR-2001; 2001GB-0007658
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteins and nucleic acid molecules from Streptococcus pneumoniae, ful as medicaments for treating or preventing a disease or infection to streptococcus bacteria, such as pneumonia, sepsis, otitis media
  printed specification, directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INST GENOMIC RES
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cc region used as a target for screening drugs useful in treatment of c diseases involving abnormal lipid metabolism including diabetic neuropathy, arterial hypertension, hypercholesteroolaemia, atherosclerotic heart disease, chronic inflammatory disorders, autoimmune disorders, c allergic eczema and other atopic disorders, inflammatory process such as rheumatoid arthritis, diminished lymphocyte proliferation, c as rheumatoid arthritis, diminished lymphocyte proliferation, c macrophage-mediated cytotoxicity, monocyte and neutrophil chemotaxis, c major histocompatibility class II expression and antigen presentation, c production of pro-inflammatory cytokines (interleukins) and 6, tumour necrosis factor) and adhesion molecule expression, eczema, psoriasis, c acute respiratory distress syndrome (ARDS), articular cartilage c degradation (ACD) and cancer. Host cell containing the control cregion of DSD gene is useful for screening for a modulator capable of regulating the expression of a mammalian DSD gene, especially for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel control region of delta-5-desaturase gene useful as a target screening compounds useful in the treatment of diseases involving abnormal lipid metabolism including diabetic neuropathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; delta-5-desaturase; D5D; drug screening; lipid metabolism; diabetic neuropathy; arterial hypertension; hypercholesterolaemia; atherosclerotic heart disease; chronic inflammatory disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human delta-5-desaturase gene control region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to human delta-5-desaturase (hD5D) gene control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 1; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         De Antueno RJ,
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09-MAR 1999

23-MAR-1999

25-MAR-1999

01-APR-1999

01-APR-1999

16-APR-1999

16-APR-1999

17-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

23-APR-1999

24-MAY-1999

05-MAY-1999

06-MAY-1999

11-MAY-1999

11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           identifying modulators that modulate lipid metabolism or diabetic neuropathy. The screening method is an assay for identifying modulators that modulate the n-3 lipid metabolic pathway, conversion of 18:3n3-22:6n3, or n-9 lipid metabolic pathway, conversion of 16:0-22:4n9 or n-6 lipid metabolic pathway, conversion of 18:2n6-22:5n6. The human D5D control region provides a powerful tool for dissecting the role of D5D gene expression and inducing modifications, which eliminate or control alterations associated with metabolic disorders. The present sequence is human delta-5-desaturase (hD5D) gene control region.
                                                                                                                                                                                                                                                                                                                                                                                                                         Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
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                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                              metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana DNA fragment SEQ ID NO: 70130.
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17; Conservative 0;
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9908-0132407

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27-MAY-1999;
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99US-0135629.
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99US-0136392.
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RESULT 17
ABV77738/c
ID ABV77738;

XX
ABV77738;

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O3-FEB-2003 (first entry)
XX

DE Human zinc finger protein 10.56
XX
Human, zinc finger protein 10.56
XX
Homo sapiens.

XX

CDS
FT C
RESULT 18
ABN69051
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28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                          The present sequence is the coding sequence for human zinc finger protein 10.56. The protein is useful for treating several diseases, such as solid tumours, nervous system disease, haemopathy, development disturbance and HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; zinc finger protein 10.56; tumour; nervous system disease; haemopathy; development disturbance; HIV infection; cytostatic; a gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human zinc finger protein 10.56 coding sequence.
                                                                                                                                                                                                          Local
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Similarity 100.0%; 1
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                                                                                            CATATTTGTCCTCCACT 221
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99US-0162142.
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99US-01470388.
99US-01477038.
99US-0147720.
99US-01477102.
99US-01477103.
99US-0147733.
99US-0148319.
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99US-0151066.
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RESULT 19
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                                                                                                                                                                                                                                                                                                      Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus/GAS (Streptococcus/GAS) (Streptococcus/GAS) (Streptococcus/GAS) (Streptococcus/GAS) (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and artibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.

Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detect Streptococcus in a CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity ing composition of immunoassays, and distinguishing/identifying
                                                                                                                                                                              Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
 AAX08433;
                                AAX08433 standard; DNA; 2264 BP
                                                                                                                                                                                                                                                           Sequence 2070 BP; 751 A; 373 C; 381 G;
                                                                                                                                                                                                                                                                                             Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a protein (ABP25413-ABP30895) from group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 7; Page 3763; 4525pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Telford J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABN69051 standard; DNA; 2070
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                                                                                                                                          CTTTATAAAGCACTCAA 24
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                                                                                                                                                                                       Conservative 0;
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                                                                                                                                                                                                       Score 17; Pred. No.
                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                         565 T; 0 other;
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67;
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                                                                                                       Query Match
Best Local S
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Ohneda M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protection of mammalian cells against immunotoxicity or lipotoxicity - used for treating, e.g. diabetes, obesity, wasting syndromes, osteoporosis, inflammatory diseases, autoimmune diseases or
                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-153448/13.
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30-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 241-242; 253pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     neurodegenerative diseases
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(TEXA) UNIV TEXAS SYSTEM.
  2047
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                                                                                  l Similarity
17; Conserv
                                                                                                                                                                          2264 BP; 634 A; 511 C; 509 G; 610 T; 0 other;
TCTACTCAGAAATTTTT 2063
                                           TCTACTCAGAAATTTTT 43
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                                                                                     Conservative
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97US-0055092
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Catalase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human kidney cells.
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                                                                                                       7.5%;
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                                                                                                          Score 17;
Pred. No.
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67;
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                                                                                                                              Length 2264;
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RESULT 21
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AC ABL88
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Best Local (
                                                                                                                                                                                                                                                                                     mammal and prophylactically used to suppress blood brain barrier disruption in a mammal having identified allergic encephalomyelitis. The rAAV composition is useful for reducing symptoms associated with demyelinating diseases such as optic neuritis, multiple sclerosis, allergic encephalomyelitis, where the symptoms associated with these disease include optic disk edema, increase of optic nerve cell count, disruption of blood brain barrier integrity, increased levels of hydrogen peroxide and demyelination of axons. The present sequence is expressed using the rAAV of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adeno-associated virus; catalase; superoxide dismutase; demyelination; optic nerve; reactive oxygen species; optic neuritis; optic disk edema; demyelinating disease; allergic encephalomyelitis; multiple sclerosis; allergic encephalomyelitis; blood brain barrier; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus (rAAV) composition. The rAAV comprises a polynucleotide sequence encoding a mammalian catalase or superoxide dismutase polypeptide to reduce demyelination in an optic nerve. The rAAV are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encephalomyelitis, comprises viral constructs expressing catalase superoxide dismutase
 16-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                               scavenging reactive oxygen species in a mammal suspected of having optic neuritis, to reduce the effects of demyelinating disease in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of recombinant adeno-associated virus composition for treating demyelinating disorders e.g. multiple sclerosis and allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
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                              ABL88432;
                                                          ABL88432 standard; cDNA; 2279
                                                                                                                                                                                                                                                            Sequence 2279 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
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(QIXX/) QI X.
(HAUS/) HAUSWIRTH W W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes the use of a recombinant adeno-associated
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                                                                                                                                                                                                 Conservative
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 (first entry)
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                                                                                                                                                                                                                                                            642 A; 514 C; 512 G; 611 T; 0 other;
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                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                               Score 17;
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RESULT 22
AAI60810
ID AAI60
AC AAI60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to identifying pain-regulating substances (A) comprises (i) incubating a test substance with a cell (or preparation from it) that has synthesised a peptide or protein (B) and (ii) measuring either binding of the test substance to (B) or some functional parameter that is altered by this binding. The method is useful for identifying pain-regulating substances (A) with analyseic activity. (A) along with nucleic acid (ABB8911-ABL88441) that encode proteins (B, ABB85006-ABB85037) that interact with (A); (B); vectors containing the nucleic acid; antibodies against (B), cells that express (B) and agents that bind to (B), are all useful for treating pain, particularly chronic pain, including use in gene therapy. The same materials can also be used for diagnosis, e.g. of neurological and neurodegenerative diseases. The present sequence is that of a polynucleotide of the invention.
                                                        peripheral nervous system, neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; SNy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                 22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                                                                                  Human polynucleotide SEQ ID NO 4799.
                                                                                                                                                                                                                                           AA160810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurodegenerative
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                                                                                                                                                                                                                                           standard; cDNA;
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Homo sapiens

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25-APR-2000;
09-JUL-2000;
         Human; nootropic; immunosuppressant; cytostatic; gene therapy; cance: peripheral nervous system; neuropathy; central nervous system; CNS; Alzhelmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                           C.N.S
                                                                                                                                                                                                                                                                                                                                                                                                       utilisation of the activities such as: Immune system suppression, activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polypucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous siguries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy Drager Syndrome. Other uses include the
                                                                                                                                                                    AAI59024 standard;
                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-AUG-2000;
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                                                                                                                  22-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                             disorders.
The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acids and polypeptides, useful as central nervous system injuries -
                                                                                       polynucleotide SEQ ID NO 1227.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; SEQ ID NO 4799; 10078pp; English
                                                                                                                                                                                                                                                                                      l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYSEQ INC.
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Wang Z,
Zhou P,
                                                                                                                                                                                                                                                                                                                                          2309
                                                                                                                                                                                                                                                    TCTACTCAGAAATTTTT 43
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; 2000US-0552317.

; 2000US-0598042.

; 2000US-0620312.

; 2000US-0623450.

; 2000US-0662191.

; 2000US-0693036.

; 2000US-07273444.
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                          BP;
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Wehrman T, X
, Goodrich R,
                                                                                                                                                                                                                                                                                                                                          654
                                                                                                                                                                    cDNA; 2318
                                                                                                                                                                                                                                                                                                                                                                               data for this patent did not form
                                                                                                                                                                                                                                                                                  100.08; --
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                                                                                                                                                                                                                                                                                                                                          521 C; 517
                                                                                                                                                                                                                                                                                                    Score 17; Pred. No.
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Xu C, Xue
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Ku C, Xue AJ,
Drmanac RT;
                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                          617 T;
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67;
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Yang
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Zhang
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                                                   cancer;
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RESULT 24
AAKS2557
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AC AAK
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19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                                                                                                                    immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/Chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang
Wang
Zhao
Human; cytokine; cell proliferation; cell differentiation; gene th vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                     06-NOV-2001
                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to human nucleic acids (AAI57798-AAI61369) the encoded polypeptides (AAM38642-AAM42213) with nootropic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 1227; 10078pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
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25-APR-2000;
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                                                                                                                                                                                                                                                                                                    disorders.
The sequence
                                              polynucleotide
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17; Conserv
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Zhou P,
                                                                                                                                                                                                                                                                    2318
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                                                                                                                  standard;
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2000US-0653450.
2000US-0662191.
2000US-0693036.
2000US-0727344.
                                                                                                                                                                                                                      larity 100.0%; I Conservative 0;
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2000US-0552317.
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                                                                     (first
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Wehrman T, X
Goodrich R,
                                                                                                                                                                                                                                                                    655
                                                                                                                  cDNA;
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                                                                     entry)
                                               SEQ ID
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                                               NO 2086.
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Xu C, Xue AJ,
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                                                                                                                                                                                                                                                                    612 T;
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67;
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Yang
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Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disorders
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RESULT 25
AAK51573
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Best Local
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27-APR-2000; 2000US-058075.
20-JUN-2000; 2000US-058075.
19-JUL-2000; 2000US-0520325.
01-SEP-2000; 2000US-062335.
15-SEP-2000; 2000US-0663561.
20-OCT-2000; 2000US-0633353.
30-NOV-2000; 2000US-0728422.
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Zhao QA,
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny inhibin activity and may be useful in the diagnosis and/or activity interests.
Human; cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; hammonodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 4467; 6221pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-FEB-2001; 2001WO-US04098
                                                                    Human polynucleotide
                                                                                                 06-NOV-2001
                                                                                                                           AAK51573
                                                                                                                                                    AAK51573 standard; cDNA; 2661
                                                                                                                                                                                                                                                                                                                                  Sequence 2652 BP; 707
                                                                                                                                                                                                                                                                                                                                                                                    inflammation.
Note: Records for SEQ ID NO 2110 (AAK52581),
                                                                                                                                                                                                                                                                                                                                                                                                                    treatment
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                                                                                                                                                                                                                                                                                                                                                          (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                                                                          Local
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DB; AAM79424.
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                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C, Drmanac RT, Asundi V, Wang D, Wang J, Zhang J, Ren Yang Y, Wejhrman T, Goodrich R;
                                                                                                                                                                                                                         TCTACTCAGAAATTTTT
                                                                                                                                                                                                                                         TCTACTCAGAAATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                  of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                              Conservative
                                                                                               (first entry)
                                                                    SEQ
                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                  A; 635 C; 635 G; 675 T; 0 other;
                                                                                                                                                                                                                                                                                           7.5%; Score 17;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                              Mismatches
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67;
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F, c
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from
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Chen
                                                                                                                                                                                                                                                                              0
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the sequence listing
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mg ZW;
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RESULT 26
ABL22534
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AC ABL22
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DT 26-MA
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20-JUN-2000; 2000US-0598075.
19-JUL-2000; 2000US-0620325.
10-SEP-2000; 2000US-0654936.
15-SEP-2000; 2000US-0663561.
20-OCT-2000; 2000US-0693325.
30-NOV-2000; 2000US-0728422.
                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM89302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activiny inhibin activity and may be useful in the diagnosis and/or restment of carear levisamia surrous surrous discounter activities.
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Zhao QA,
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27-APR-2000; 2000US-0560875
20-JUN-2000; 2000US-0598075
            Drosophila melanogaster
                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                                                                                                 Sequence 2661 BP; 713 A; 638 C; 637 G; 673 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 765-767; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding polypeptides with cytokine-like useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB;
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                                      pharmaceutical;
                                                     Drosophila;
                                                                             Drosophila
                                                                                                                                  ABL22534;
                                                                                                                                                           ABL22534 standard;
                                                                                                                                                                                                                                                                                                                                                        (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                                                                                                                                                                                               treatment of cancer, leukaemia,
                                                                                                                                                                                                                                                                                                                                                                                    Note: Records for SEQ ID NO 2110 (AAK52581),
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                                                                                                                                                                                                                                                                                                                                                                                                   inflammation.
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DB; AAM78440.
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                                                                                                                                                                                                                                                                              l Similarity
17; Conserv
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, Wang D,
Yang Y,
                                                                                                                                                                                                                                                     TCTACTCAGAAATTTTT 43
                                                                                                                                                                                                                            TCTACTCAGAAATTTTT 2431
                                                                             melanogaster genomic polynucleotide
                                                     developmental
                                                                                                                                                                                                                                                                                Conservative
                                                                                                       (first entry)
                                      gene;
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, Zhang J, Ren
n T, Goodrich R,
                                                   biology;
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Pred. No.
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                                                     cell
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67;
                                                    signalling;
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Chen
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Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and content of the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid
genes from Drosophila and
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11-JUL-2000; 2000US-0614150.
                                                               23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                                                        Drosophila melanogaster genomic polynucleotide SEQ ID NO 17650
                                                                                                                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                                                                                                            ABL22059 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2662 BP; 748 A; 596 C; 604 G; 714 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 19075; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001; 2001WO-US09231.
WPI; 2001-656860/75
                     Venter JC,
                                                                                                23-MAR-2001; 2001WO-US09231.
                                                                                                                                             WO200171042-A2
                                                                                                                                                                                        pharmaceutical;
                                                                                                                                                                                                   Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                      ABL22059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             specification,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence data for this patent did not form cification, but was obtained in electronic f
                                                                                                                                                                                                                                                                                                                                                     1062
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                     Adams M,
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Pred. No.
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novel

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gland antigen, Seq ID No

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                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.
21-NOV-2001
                                                              AAS30407 standard;
                                                                                                                                                                                                                                                                   Sequence 5790 BP; 1480 A; 1401 C; 1414 G; 1495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 17650; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes from Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
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                                                                                                                                            CTGGATTTTCTACCCGG
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(first
                                                              DNA; 6352
entry)
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Pred. No.
                                                              ВP
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osteopathic; prostate gland; prostatitis; adenocarcinoma; hair loss; prostatosis; malacoplakia; adenocarcinoma; benign prostatic hypertrophy; hyperplasis; carcinoma; prostate neoplastic disorder; skin aging; reproductive system disorder; autoimmune disorder; urinary system; systemic lupus erythematosus; rheumatoid arthritis; cardiovascular; blood-related disorder; hyperproliferative disorder; respiratory; neurological disorder; hyperproliferative disorder; respiratory; liver disorder; wound healing; food preservative; ds. antiarthritic; antirheumatic; virucide; hepatotropic; nephrotropic; antianaemic; dermatological; immunosuppressive; antiinflammatory; Human; nootropic; neuroprotective; cytostatic; antiparkinsonian Homo sapiens.

02-AUG-2001

02-MAR-2000; 116-MAR-2000; 117-MAR-2000; 18-APR-2000; 19-MAY-2000; 07-UUN-2000; 28-UUN-2000; 30-UUN-2000; 07-UUL-2000; 17-JAN-2001; 2001WO-US01330. 24-FEB-2000; 2000US-0186350. 2000US-019974. 2000US-0199076. 2000US-0199123. 2000US-0205515. 2000US-0205467. 2000US-0214886. 2000US-0215135. 2000US-0184664. 2000US-0180628 2000US-0179065

2000US-0217496.
2000US-0217496.
2000US-0220963.
2000US-022964.
2000US-0225218.
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2000US-02252770.
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2000US-0225758.
2000US-0225759.
2000US-0225759.
2000US-0225759.

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20-OCT-2000
01-NOV-2000
08-NOV-2000
017-NOV-2000
117-NOV-2000
117-NOV-200
The invention relates to novel isolated prostate gland related nucleic acids (I) and polypeptides (II). (I) and (II) are useful for diagnosis, prognosis, prevention, and/or treatment of diseases and/or disorders of the prostate such as acute non-bacterial prostatitis, chronic non-bacterial prostatitis, acute bacterial prostatitis, prostatodystonia, prostatosis, granulomatous prostatitis, malacoplakia, benign prostatic hypertrophy or hyperplasia, and prostate neoplastic disorders, including adenocarcinomas, transitional cell carcinomas, ductal carcinomas, and squamous cell carcinomas. (I), (II) and antibody to (II) are useful for
                                                                                                                                                                                                                                                          Novel isolated prostate gla
and treatment of disorders
prostatosis, prostatitis, l
                                                                                                                                                                                                      Claim
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2000US-02511868.
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11-JUL-2000
11-JUL-2000
12-JUL-2000
12-JUL-2000
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2000US-022868 2000US-0227109 2000US-02271182 2000US-022934 2000US-022934 2000US-022934 2000US-022934 2000US-0231243 2000US-0231243 2000US-0231413 2000US-0231413 2000US-0231413 2000US-0232081 2000US-0232081 2000US-0232081 2000US-0232081 2000US-0232081 2000US-0232081 2000US-0232081 2000US-0232981 2000US-0232981 2000US-0232981 2000US-0232993 2000US-0232993 2000US-0232993 2000US-0234274 2000US-0234293 2000US-0234293 2000US-0234293 2000US-0234293 2000US-0234293 2000US-0234293 2000US-0234293 2000US-0234293 2000US-0234293 2000US-0235884 2000US-0235884 2000US-0235884 2000US-0235884 2000US-0235884 2000US-0235886 2000US-0235886 2000US-0235886 2000US-0235886 2000US-0235886 2000US-0235886 2000US-023680 2000US-02

malacoplakia

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12-MAR-2000

17-MAR-2000

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18-APR-2000

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07-JUL-2000

07-JUL-2000

07-JUL-2000

11-JUL-2000

14-JUL-2000

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14-JUL-2000

14-AUG-2000

14-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosing and treating reproductive system disorders (Paget's disease), autoimmune disorders (systemic lupus erythematosus, rheumatoid arthritis), blood-related disorders (sickle cell anaemia), hyperproliferative disorders (sickle cell anaemia), hyperproliferative disorders, usinary system disorders, neural activity and neurological disorders (musculoskeletal system disorders, neural activity and neurological disorders (Alzheimer's disease and Parkinson's disease), endocrine disorders (Addison's disease), gastrointestinal disorders (inflammatory disorders), liver disorders (biliary liver cirrhosis), pancreatic and gall bladder disorders, disorders of the large intestine, developmental and inherited disorders, disorders at the cellular level, and wound healing and epithelial cell proliferation. (I) or (II) is useful to prevent skin aging, for preventing hair loss, to maintain
                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
24-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                17-JAN-2001; 2001WO-US01339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human
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           2000US-0217496

2000US-0218290

2000US-022964

2000US-022964

2000US-0224518

2000US-0224519

2000US-0225211

2000US-0225214

2000US-0225266

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2000US-0225267
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2000US-0198123.
2000US-0205515.
2000US-0209467.
2000US-0214886.
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2000US-0216647.
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2000US-0217487.
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2000US-0184664.
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Pred. No.
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RESULT 30
ABL14618
ID ABL14
XX
AC ABL14
XX
AC ABL14
XX
AC ABL14
XX
AC ABL16
AC ABL16
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AC ABC16
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17-NOV-2000;
17-NOV-2000;
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08-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be use in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding protein of the invention.
                Drosophila melanogaster expressed polynucleotide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen
                                                    26-MAR-2002
                                                                                       ABL14618;
                                                                                                                        ABL14618 standard; cDNA; 6829
                                                                                                                                                                                                                                                                                                                                                    Sequence 6352 BP; 1925 A; 1111 C; 1393 G; 1923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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   23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genomic polynucleotide SEQ ID NO 17647.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
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                                                                                                                                                                                                                                                                                                      Human; lipid metabolism protein; nootropic; neuroprotective; cardiant; cerebroprotective; hepatotropic; antidiabetic; ophthalmic; nephrotropic; immune disorder; autoimmune disease; rheumatoid arthritis; glossitis; systemic lupus erythematosus; conjunctivitis; inflammatory disorder; systemic lupus erythematosus; conjunctivitis; inflammatory disorder; respiratory disorder; asthma; allergy; CNS disorder; Alzheimer's disease; parkinson's disease; atheroselerosis; cardiovascular disorder; cancer; coronary disease; familial hypercholesterolaemia; hyperlipidaemia; haematopoietic disorder; hypolipidaemia; lipidosis; Gaucher's disease; Tay-sach's disease; mental retardation; gene therapy; antisense therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in lucidating cell signalling and cell-cell interactions in higher eukaryotuces for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01876-ABL30511), expressed DNA sequences (ABL01870-ABL16175) and the encoded proteins (ABB573737-ABB72072).
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2000US-0217487.
2000US-0218290.
2000US-022963.
2000US-0224518.
2000US-02254519.
2000US-0225213.
2000US-0225214.
2000US-0225266.
2000US-0225266.
2000US-0225267.
2000US-02252757.
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18-DEC-2000;
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 31-JAN-2000

04-FEB-2000

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16-MAR-2000

11-MAR-2000

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l similarity 100.0%;
17; Conservative (
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atic; gene therapy; vaccine; metastasis; ds.
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2000US-025929
2000US-0179065

2000US-0186628

2000US-0186350

2000US-019874

2000US-0198123

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2000US-0246477.
2000US-0246478.
2000US-0246523.
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2000US-0246526.
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A ARE AREARE AREAR AREAR
                                  CC amino acid sequences given in AAM82170 to AAM879291. (I) have cytostatic contivity, and can be used in gene therapy and vaccine production. (I) controlled and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For cexample, they may be used to treat disorders associated with decreased cexpression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to controlled acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting contein. (I) proteins and polynucleotides may be used to prevent, concers and treat immune/haematopoietic-derived cells. AAK64703 concers and cancer metastases of haematopoietic antigen genomic concers from the present invention. AAK54942 to AAK54950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
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2000US-0251479.
2000US-0251856.
2000US-0251869.
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RESULT 34
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ADAK844865
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31-JAN-2000
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24-FEB-2000
16-MAR-2000
17-MAR-2000
17-MAR-2000
19-MAY-2000
07-JUN-2000
07-JUL-2000
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cytostatic; gene therapy; vaccine; metastasis; ds.
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2000US-0179065.
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2000US-0199076.
2000US-0299457.
2000US-0214886.
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2000US-0214886.
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2000US-0228514.
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2000US-0225275.
2000US-02257577.
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2000US-023935.
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AAK84864
ID AAK84
XX AAK84
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                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic cactivity, and can be used in gene therapy and vaccine production. (I) creatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disporders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the proteins and polymucleotides may be used to provent, and diagnose and treat immune/haematopoietic related diseases, especially cancers and cancer metastases of haematopoietic antigen genomic to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK84950 and AAM82169
                                                                                                                                                                                                                                                                                                                                      Best
                                                                                                                                                                                                                                                                                                                  Matches
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01-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding useful for preventing, metastasis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAK54951 to AAK64702 encode the human immune/haemat amino acid sequences given in AAM82170 to AAM91921.
Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                  Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39676.
                                                                           07-NOV-2001
                                                                                                              AAK84864;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23527 BP; 6788 A; 5333 C; 5424 G; 5982 T; 0 other;
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                                                                                                                                                AAK84864 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                               represent sequences used
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17; Conserv
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2000US-0251030

2000US-0251479

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2000US-0251486

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2000US-0251869

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                                                                       (first entry)
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                                                                                                                                                DNA;
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                                                                                                                                                                                                                                                                                                                                    Score 17;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM
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67;
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 XXOXEX COXEX COXE COCCEC COCCECCEC COCCEC COCCECCA COCCEC COCCECC
                                                  14-AUG-2000
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01-SEP-2000
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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19-MAY-2000;
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                                                  2000US-0230437

2000US-0231242

2000US-0231243

2000US-0231244

2000US-0231413

2000US-0231414

2000US-0231414

2000US-0232141

2000US-0232141

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2000US-0189874.
2000US-0190076.
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2000US-0224518
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2000US-0229287.
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2000US-0225759
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2000US-0225270.
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2000US-0220963
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25-SEP-2000; 26-SEP-2000; 27-SEP-2000; 27-SEP-2000;

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2000US-0251856.
2000US-0251868.
2000US-0251869.
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2000US-0244617.
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2000US-0249215.
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2000US-0246611.
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RESULT 36
AAV52155
ID AAV52
AC AAV52
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae; computer readable medium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae genome fragment SEQ ID NO:22.
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  Computer-readable medium with recorded Streptococcus pneumoniae
                                                        WPI; 1998-272225/24
                                                                                                                                                                                                                                                            31-OCT-1996;
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                                                                                                                                                                                                                                                                                                                                                                            07-MAY-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae
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                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
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                                                                                                                   Choi GH,
Rosen CA;
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                                                                                                                                                                                                                                                            96US-0029960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S. pneumoniae; genome; diagnosis; assay; vaccine; pharmaceutical composition; ds.
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; Pred. No. 67;
0; Mismatches
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                                                                                                                                              Dougherty BA,
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67;
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20-CT-2000
02-CT-2000
03-NCV-2000
04-NCV-2000
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09-NCV-2000
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01-NCV-2000
01-NCV-2000
01-NCV-2000
01-NCV-2000
01-DEC-2000
01-DEC-2000
01-DEC-2000
08-DEC-2000

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RESULT 37
AAL36829/c
ID AAL36829
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Best Local S
Matches 17
31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA, DNA or cDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. resuments of the S. resuments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members or (b) isolating
                                                                                                                                                                                                                                                                                                            Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
                                                                                                                                                                                                                                                                                              cardiant; gene therapy; cancer; immune disorder; cardiova neurological disease; infection; human; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ
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SEQ ID NO:1 to 391 (AAV5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes a computer readable medium which has nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV52524) nucleotide sequence at least orded on it, or a representative fragment or a sequence at least ntical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted ID NO: 1 to 391 (AAV52134 to AAV52524) are genomic fragments from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8669
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Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.

Example 2 IJ ö 3194; 781pp + Sequence Listing; English

for preventing, protein or gene The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human

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RESULT 38
ABX59817/c
ID ABX5981
XX ABX5981
AC ABX5981
XX CFEB
XX CGene;
XX GGene;
XX G
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   31-JAN-2000;

04-FEB-2000;

28-JUN-2000;

07-JUL-2000;

07-JUL-2000;

11-JUL-2000;

11-JUL-2000;

14-JUL-2000;

26-JUL-2000;

14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene; ss; musculoskeletal system antigen; cancer; metastasis; re-vascularisation; thrombosis; arteriosclerosis; mineral content; cardiovascular condition; wound; injury; burn; anglogenesis; ulcer; post-operative tissue repair; limb regeneration; neuronal growth;
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Note: The sequence da
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14-AUG-2000
114-AUG-2000
22-AUG-2000
01-SEP-2000
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14-AUG-2000;
14-AUG-2000;
          and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers; stimulates angiogenesis and limb regeneration; stimulates neuronal growth; can treat and prevent neuronal damage occurring in certain disorders or neurodegenerative conditions, such as, Alzheimer's disease, Parkinson's disease, and AIDS-related complex; stimulates chondrocyte growth, thus they can be used to enhance bone and periodontal regeneration and aid in tissue transports or bone grafts; prevents skin aging due to subcurn by stimulating keratinocyte growth; prevents hair loss, since FGF family members activate hair-forming cells and promotes melanocyte growth; stimulates growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines; maintains organs before transplantation or for supporting cell culture of primary tissues; induces tissue of mesodernal origin to differentiate in early
                                                                                                                                                                                                                                                                                     The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and ather associated with conditions such as thrombosis, arteriosclerosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecules associated polypeptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ROSE/)
(RUBE/)
(BARA/)
                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 3194; 321pp; English
                                                                                                                                                                                                                                                                                                                                                                        invention describes an isolated nucleic acid molecule comprising
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RUBEN S
BARASH
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2000US-22526RP.
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2000US-22575RP.
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2000US-225937P.
2000US-225934P.
2000US-229343P.
2000US-229345P.
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2000US-23423P.
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2000US-23423P.
2000US-234597P.
2000US-23636P.
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2000US-236370P.
2000US-237039P.
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2000US-237039P.
2000US-241709P.
2000US-244709P.
2000US-244617P.
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increases

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decreases

the differentiation

or proliferation

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RESULT 39
AAL3683/c
ID AAL368
AC AAL368
AC AAL368
AC AAL368
AC AAL368
AC Cytost
KW Cytost
KW cardia
KW reardia
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CC mammalian characteristics, such as, body height, weight, hair colour, eye
CC colour, skin, percentage of adipose tissue, pigmentation, size, and shape
CC (e.g., cosmetic surgery); modulates mammalian metabolism; changes
CC mammal's metal state or physical state by influencing biorhythms,
CC caricadic rhythms, depression, tendency for violence, tolerance for pain,
CC reproductive capabilities, hormonal or endocrine levels, appetite,
CC libido, memory, or stress; increases or decreases storage capabilities,
CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors
CC or other nutritional components. This sequence encodes a novel human
CC musculoskeletal system antigen.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from the US patent office at
CC fitp.seqdata.uspto.gov/sequence.html?DocID=20020147140.
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31.JAN-2000;
04.FEB-2000;
24.FEB-2000;
02.MAR-2000;
16.MAR-2000;
11.MAR-2000;
11.JUN-2000;
07.JUN-2000;
07.JUL-2000;
07.JUL-2000;
07.JUL-2000;
11.JUL-2000;
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2000US-0186350
2000US-019874
2000US-0199123
2000US-0199123
2000US-0209467
2000US-0219486
2000US-0214886
2000US-0214886
2000US-0214887
2000US-0214887
2000US-0216880
2000US-022963
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2000US-0180628.
2000US-0184664.
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The invention relates to novel genes (AAL34669-AAL37666) and proteins CC (ABB03087-ABB04109) associated with the musculoskeletal system useful CC for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human CC tissues disclosed in the specification. The nucleic acids, proteins, cc antibodies and (ant)agonists are useful in the diagnosis, treatment CC antribodies and (ant)agonists are useful in the diagnosis, treatment CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and CC other cancers of the adrenal gland, bone, bone marrow, breast, CC gastrointestinal tract, liver, lung, or urogenital; (b) immune CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as wyocardial ischaemias; (d) wound CC parasitic infections.
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08.NOV-2000
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11.NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g. diagnosis -
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2000US-0246525

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2000US-0249207

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2000US-0249211

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2000US-0249214

2000US-0249214

2000US-0249216

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2000US-0251989
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14 AUG 2000
16 AUG 2000
22 AUG 2000
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24 AUG 2000
25 SEP 2000
06 SEP 2000
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2000US-022524 2000US-022526 2000US-022526 2000US-022575 2000US-022575 2000US-022575 2000US-022575 2000US-0226681 2000US-022700 2000US-022700 2000US-022824 2000US-02394 2000US-02394 2000US-02394 2000US-023124 2000US-023126 2000

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Best Local
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
22-AUG-2000;
22-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
                                                                                                                                                            26-JUL-2000;
26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        post-operative tissue repair; limb regeneration; neuronal growth; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; AlDS-related complex; chondrocyte growth; bone regeneration; periodontal regeneration; tissue transport; bone graft; skin aging; keratinocyte growth; hair loss; melanocyte growth; cell proliferation; cell growth; organ transplant; cell differentiation; body height; weight; hair colour; eye colour; skin; percentage of adipose tissue; pigmentation; cosmetic surgery; metabolism; blorhythm; caricadic rhythm; depression; tendency for violence; pain; reproductive capability; hormone level; endocrine level; appetite; libido; memory; stress; storage capability; fat content; lipid content; protein content;
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11-JUL-2000;
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07-JUL-2000;
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28-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                 14-JUL-2000;
                                                                                                                                                                                                                                                                                                              31-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                              US2002147140-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 carbohydrate content; vitamin content; cofactor content;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA encoding novel human musculoskeletal system antigen #2165.
                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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17; Conserv
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         7 2000US-179065P

2000US-180628P

2000US-214868P

2000US-216647P

2000US-217487P

2000US-217487P

2000US-217496P

2000US-221964P

2000US-220964P

2000US-224518P

2000US-224518P

2000US-225568P

2000US-225568P

2000US-225768P

2000US-225768P

2000US-225768P

2000US-225757P

2000US-225758P

2000US-225758P

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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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67;
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21-SEP-2000;
27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
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02-OCT-2000;
02-OCT-2000;
02-OCT-2000;
03-OCT-2000;
04-OCT-2000;
05-OCT-2000;
06-OCT-2000;
07-OCT-2000;
07-OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated nucleic acid molecules encoding musculoskeletal system associated polypeptides, useful for detecting disorders, e.g. {\it c.g.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 3198; 321pp; English.
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) RUBEN S M.
) BARASH S C
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2000US-236367P
2000US-236368P
2000US-236369P
2000US-236370P
2000US-236370P
2000US-237037P
2000US-237038P
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2000US-251856P.
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2000US-244617P.
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2000US-240960P.
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cancer

CC conditions, such as, Alkheimer's disease, Parkinson's disease, and CC conditions, such as, Alkheimer's disease, Parkinson's disease, and CC used to enhance bone and periodontal regeneration and aid in tissue CC transports or bone grafts; prevents skin aging due to sunburn by CC stimulating keratinocyte growth; prevents hair loss, since FGF family CC stimulates growth and differentiation of hematopoietic cells and bone CC organs before transplantation or for supporting cell culture of primary CC embryos; increases or decreases the differentiation or proliferation of embryonic stem cells, besides, haematopoietic lineage; modulates growth; cells used body height, weight, weight, weight, weight, hair colour, eye CC colour, skin, percentage of adipose tissue, pigmentation, size, and shape CC (e.g., cosmetic surgery); modulates mammalian characteristics, such as, body height, weight, hair colour, eye CC (e.g., cosmetic surgery); modulates mammalian metabolism; changes CC mammal's metal state or physical state by influencing biorhythms, creptoductive capabilities, hormonal or endocrine levels, appetite, CC reproductive capabilities, hormonal or endocranes storage capabilities, cofactors CC fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors CC mincrollekeletal existem antigen. The invention describes an isolated nucleic acid molecule comprising a sequence encoding musculoskeletal system associated polypeptides useful for detecting disorders, e.g., cancer or cancer metastases, in animals or humans. The nucleic acid: stimulates re-vascularisation of ischaemic tissues associated with conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions; treats wounds due to injuries, burns, post-operative tissue repair, and ulcers, stimulates angiogenesis and limb regeneration; stimulates neuronal growth; can treat and prevent neuronal damage occurring in certain disorders or neurodegenerative conditions. musculoskeletal system antigen.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly

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ABL18664/c
ID ABL186
XX ABL186
XX ABL186
XX Drosop
XX WO2001
XX Drosop
XX WPI;
XX WPI;
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PT Genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 41
                                                                                                        Matches
                                                                                                                          Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid genes from Drosophila and
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ftp.seqdata.uspto.gov/sequence.html?DocID=20020147140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                        Sequence 30143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-656860/75
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                                                                                                                                                                                                                                                                                     specification,
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11695
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                                                                                                                                                                                                                                                                                sequence data for this patent did not form part of the printed cification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity
17; Conserv
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17; Conserv
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ک
CTACCGATTTTCTATTT 11679
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                             CTACCGATTTTCTATTT
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                                                                                                     Conservative
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                                                                                                                                                                                                        BP; 8018 A; 6821 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                  Score 17; DB; Pred. No. 67; 0; Mismatches
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Pred. No.
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67;
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67;
                                                                                                                                                                                                        8882 T; 0 other;
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RESULT 42
                                                                                                                                                                                                                 in which the corresponding protein is preferentially expressed. The transporter proteins isolated from humans and their human/mammalian orthologues serve as targets for identifying agents for use in mammalian therapeutic applications, and biological assays related to transporter proteins that are related to members of the GABA neurotransmitter transporter subfamily. The proteins and peptides also provide a target for diagnosing a disease or predisposition to disease mediated by the peptide, and are useful for treating a disorder characterised by absence of, inappropriate, unwanted or altered expression of the protein. The antibodies are also useful for assessing normal and aberrant subcellular
                                                        localisation of cells in various tissues in an organism, in pharmacogenomic analysis, for tissue typing and for inhibiting protein function. (II) is useful for constructing recombinant vectors, host cells and transgenic animals; for designing ribozymes; in drug screening; in diagnostic assays for qualitative changes in gene expression, particularly in qualitative changes that lead to pathology; in gene therapy; and to detect mutations in genes encoding transporters. This sequence encodes a novel human aminobutyric acid (GABA) transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human transporter protein, related to gamma-aminobutyric acid neurotransmitter transporter subfamily useful as model for developing human therapeutic targets and serves as target for human therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                           development of human therapeutic agents that modulate transporter activity. (I) is used to raise antibodies or to elicit another immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, and as markers for tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is related to the gamma-aminobutyric acid (GABA) neurotransmitter transporter subfamily. (1) and the nucleic acid encoding it (1) can be used as models for the development of human therapeutic targets, aid in the identification of therapeutic proteins and serve as targets for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-102517/09.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; gamma-aminobutyric acid; GABA; neurotransmitter transporter; transgenic animal; ribozyme design; drug screening; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomic DNA encoding novel human GABA transporter related protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABX61804 standard; DNA; 40645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention describes an isolated human transporter peptide (I) that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Fig 3; 114pp; English.
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(KETC/)
(DFRA/)
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KETCHUM K A.
DI FRANCESCO
BEASLEY E M.
                                            protein.
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                     CC GC, where differential expression of Gs is indicative of GCA.

CC Also included are modulating (M2) GA by contacting GC with an agent CC that alters the expression of at least one gene in Gs; (2) screening (M3) CC for an agent capable of modulating GCA or an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease using the CC gene expression profile; (3) detecting (M4) an inflammation (especially CC chronic) in a tissue, an allergic response in a subject, exposure of a CC subject to a pathogen or sterile inflammatory disease, by detecting the CC level of expression in a sample of the tissue of gene(s) from Gs, where CC the level of expression of the gene is indicative of inflammation, (M5) an inflammation (especially chronic) or in a tissue, CC an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having CC inflammation with an agent that modulates the expression of gene(s) from GS in the tissue. M1 is useful for detecting GCA, M2 is useful for CC modulating GA; M3 is useful for screening an agent capable of modulating CC detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject on a pathogen or sterile inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject on spathogen or sterile inflammatory disease (a capacially chronic) in a tissue, an allergic inflammatory disease (a capacially chronic) and pathogen or sterile inflammatory disease (a capacially chronic) in a tissue, an allergic inflammatory disease (a capacially chronic) in a pathogen or sterile inflammatory disease (a capacially chronic) in a tissue, an allergic inflammatory disease (a capacially chronic) in a tissue, an allergic inflammatory disease (a capacially chronic) in a tissue or sterile inflammatory disease (a capacially chronic) in a tissue or sterile inflammatory di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-2000; 2000US-237189P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         granulocyte activation; chronic inflammation; allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fungal infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chip analysis as given in the specification, and comparing expression level to an expression level in an unactivated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146; 114pp; English.
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patient, which comprise detecting the level of expression in a tissue sample of two or more genes selected from those shown in ABT09867-ABT11112, where a differential expression of the genes indicates breast cancer. The methods are useful in diagnosing, treating, detecting the progression, and in monitoring treatment of breast cancer in patients. The methods are also useful as a screening tool for agents that modulate the onset or progression of breast cancer. The breast cancer genes may be used as diagnostic markers for the prediction or identification of the malignant state of breast tissue, for confirming the type and progression of cancer, and for drug screening and assays. The present sequence is a coding sequence of the invention.

Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis periodontal disease; also bacterial infection, viral infection parasitic infection, protozoal infection, fungal infection and useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granuloc Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diagnosing breast cancer in a patient comprises detecting the level of gene expression in cell or tissue samples, where a differential gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-674803/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Orr MS,
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25-APR-2001; 2001US-286090P
23-MAY-2001; 2001US-292517P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; breast specific gene; breast cancer; differential expression; cytostatic; gene therapy; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 281; 260pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expression is indicative of breast cancer
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                                                                                                                                                                                                                                                                                                                                                            The present invention relates to methods of diagnosing breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENE-) GENE LOGIC INC.
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                                                            The invention relates to a novel isolated peptide comprising or CC consisting of an amino acid sequence selected from an amino acid sequence cof a variant oestrogen receptor protein (e.g. ERbeta), or a fragment of CC 10 amino acids), antibodies against them, nucleic acids encoding CC them (including vectors for transforming calls). The gene for human CC ERbeta is located on chromosome 6q.25.1. The variant peptides and CC proteins can be used in assays to determine the biological CC cactivity of the protein, to raise antibodies, as a reagent in assays CC designed to quantitatively determine levels of the protein in CC collogical fluids, to identify compounds that modulate receptor CC activity and to screen compounds for the ability to stimulate or CC inhibit interacts with the receptor protein and a target molecule CC that normally interacts with the receptor protein, e.g. oestrogen. CC that normally interacts with the receptor protein, to assess expression in CC disease states e.g. cardiovascular disease and autoimmune disease (e.g. Cartenorous).
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Best Local
          osteoporosis, breast cancer and endometrial cancer. In addition the antibodies can be used in pharmacogenomic analysis and inhibiting protein function, e.g. blocking the binding of the oestrogen receptor
                                                                                                                                                                                                                                                                                                                                                                                                                      Oestrogen receptor gene and protein polymorphisms useful for diagnosis of individuals at risk of developing bone disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; Oestrogen receptor beta; ERbeta; ds; SNP; chromosome 6q.25.1; single nucleotide polymorphism; cardiovascular disease; autoimmune disease; systemic lupus erythematosus; arthritis; rheumatism; osteoarthritis; osteoporosis; breast cancer; endometrial cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub.published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 185035 BP; 42256 A; 51727 C; 51210 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-FEB-2000; 2000US-0183755.
24-JAN-2001; 2001US-0768185.
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partner such as
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100.0%; Pred. No.
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Query Match
Best Local Similarity
Matches 17; Conserv
                                                         Sequence 325791 BP; 94098 A; 68292 C; 67970 G; 95431 T; 0 other
                                                                                  human ERbeta gene.
                                                                                                 encoding the proteins can be used as probes, primers, chemical intermediates and in biological assays. The present sequence is the
  Conservative
              100.0%;
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  Mismatches
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67;
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Search completed: February 4, 2004, 15:29:44
Job time : 291 secs

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165554 ATGGCCTTAAGTTCCTC 165570

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seq length: 2000000000
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Match
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/FCTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-09-107-532A-248
US-09-126-109-9
US-09-626-312D-916
US-09-626-312D-916
US-08-661-527-2
US-09-313-294A-6323
US-09-702-705-13
US-09-736-457-13
US-09-736-457-46
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US-09-205-258-67
US-09-21-702B-188
US-09-23-313D-1
US-09-679-409-1
US-09-679-409-1
US-09-221-017B-254
US-09-221-017B-254
US-09-232-313D-1
US-09-107-532A-1108
US-09-784-508-3
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        Sequence 248, App
Sequence 916, App
Sequence 916, App
Sequence 62, Appl
Sequence 1614, Ap
Sequence 1614, Ap
Sequence 114, Ap
Sequence 114, Ap
Sequence 13, Appl
Sequence 13, Appl
Sequence 794, App
Sequence 794, App
Sequence 188, Appl
Sequence 188, Appl
Sequence 188, Appl
Sequence 1, Appli
Sequence 254, Appl
Sequence 254, Appl
Sequence 51, Appli
Sequence 1108, Appl
Sequence 15, Appl
Sequence 3, Appli
Sequence 2461, Appli
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RESULT 1 US-09-107-532A-248 JSequence 248, Application US/09107532A Sequence 248, Application US/09107532A Sequence 248, Application US/09107532A Sequence 248, Application US/09107532A PATELT NO. 6583275 PATELT NO. 6583	28 15 6.6 1886 4 US-08-936-165A-224 Sequence 224, App 1 5 6.6 2042 2 US-08-933-821-16 Sequence 16, Appl 2 C 29 15 6.6 2042 3 US-08-934-494-5 Sequence 16, Appl 2 C 31 15 6.6 2042 3 US-08-960-507-16 Sequence 5, Appl 2 C 32 15 6.6 2042 4 US-09-143-068-5 Sequence 5, Appl 2 C 34 15 6.6 2042 4 US-09-202-089-5 Sequence 5, Appl 2 C 37 15 6.6 2042 4 US-09-318-828-16 Sequence 16, Appl 2 C 37 15 6.6 2042 4 US-09-313-928A-16 Sequence 16, Appl 2 C 39 15 6.6 2042 4 US-09-313-928A-16 Sequence 16, Appl 2 C 40 15 6.6 2042 4 US-09-313-929-16 Sequence 16, Appl 2 C 41 15 6.6 2042 4 US-09-332-929-16 Sequence 16, Appl 2 C 42 15 6.6 2042 4 US-09-332-929-16 Sequence 16, Appl 3 C 42 15 6.6 2042 4 US-09-333-075-16 Sequence 5, Appl 3 C 44 1 15 6.6 2042 4 US-09-333-075-16 Sequence 5, Appl 3 C 45 1 15 6.6 2042 4 US-09-333-075-16 Sequence 16, Appl 3 C 45 1 15 6.6 2042 4 US-09-333-075-16 Sequence 16, Appl 3 C 45 1 15 6.6 20
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LOCATION: (B) LOCATION 1...1896

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                                        Query Match
Best Local Similarity
Matches 17; Conserv
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Patent No. 61
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2264 base pair
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APPLICATION NUMBER: US 60/
FILING DATE: 30-JUL-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US UNA
FILING DATE: 03-MAR-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                          TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/126,109 FILING DATE: 30-UUL-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rhodes, Christon
APPLICANT: Hugl, Sigrun R.
APPLICANT: Cousin, Sharon
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: TO NO-N
                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (512) 418-3000
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                                                                                                                                                                                                                                                                                 NAME: McMillian, Nabeela R. REGISTRATION NUMBER: P-43,3 REFERENCE/DOCKET NUMBER: UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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27 TCTACTCAGAAATTTTT 43
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P.O. Box 4433
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Hohmeier, Hans-Ewald
Newgard, Christopher B.
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Shimabukuro, Michio
                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                             US Unknown
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                                                              Score 17; DB 3; Pred. No. 7.3;
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                                                                          Length 2264;
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APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 658962el Nucleic Aci
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SOFTWARE: pt_FL_genes Version 1.0
LENGTH: 2318
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; NAME/KEY: CDS
; LOCATION: (103)..(1686)
US-09-620-312D-916
                                                                                                                                                                                                                                                                                             US-08-961-527-22
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Patent No. 6420135
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
                                                                                                                                                                                     TITLE OF INVENTION: Streptococcus
NUMBER OF SEQUENCES: 391
                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         APPLICANT: Charles Kunsch
TITLE OF INVENTION: Strep
                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 17; Conserv
OPERATING SYSTEM:
                                                                               COUNTRY:
                                                                                                                                                     ADDRESSEE:
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                                                                                                Rockville
maryland
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Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
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Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
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                                                                                                                                      9410 Key West Avenue
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                                                                                    USA
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MSDOS version 6.2
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100.0%; Pred. No.
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SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/961,527 FILING DATE:

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LELICANT: Sherman, Bradley K.

FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 6323
LENGTH: 300
Typp: ....
                      RESULT 6
US-09-702-705-1614/c
US-09-702-705-1614, Application US/09702705
; Patent No. 6504010
; Patent No. 6504010
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TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 28171 base pairs
                  GENERAL INFORMATION:
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                                                                                                                                                                                          Matches
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   APPLICANT:
                                                                                                                                                                                                                                                                 NAME/KEY: unsure
LOCATION: 92, 254, 257, 294
OTHER INFORMATION: a, t, c,
                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700351604H1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Brookes, A. Anders REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 28171 base pairs
TYPE: nucleic acid
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                                                                                                                              144 CTTGCCTCGTATTGTC
                                                                                                                                                          122 CTTGCCTCGTATTGTC 137
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Wang, Tongtong
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100.0%; Pred. No.
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RESULT 8
US-09-702-705-13
; Sequence 13, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:

APPLICANT: Wang, Tongtong

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APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILLING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 183
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1614
LENGTH: 439
TYPE: DNA
ORGANISM: Homo sapiens
US-09-702-705-1614

7.0%; Score 16; DB 4
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В
                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-1614
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                                                                                                                                                               FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1614
LENGTH: 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFO
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1614, Application US/09736457 Patent No. 6509448
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                                                            Matches
                                                                           Query Match
Best Local :
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                                                                                                                                                                                                                                                         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478015
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                                                                       Local Similarity
193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION:
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                      212 GTCCTCCACTTTCACA 227
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16; Conserv
                                                            16;
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Carter, Darrick
Retter, Marc
Mannion, Jane
                                                                                                                                                                                                  FastSEQ for Windows Version 3.0
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Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
GTCCTCCACTTTCACA
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Wang, Aijun
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Lodes, Michael A.
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Lodes, Michael A.
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178
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Pred. No. 24;
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CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
LENGTH: 493
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(493)
OTHER INFORMATION: n = A,T,C or G
US-09-736-457-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 493
; TYPE: DNA
; ORGANISM: Homo sapien
; PEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(493)
; OTHER INFORMATION: n = A,T,C or G
US-09-702-705-13
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US-09-736-457-13
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                                                            Query Match
Best Local Similarity
Matches 16; Conserv
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SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 13, Application US/09736457 Patent No. 6509448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C1.4
CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILLING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REPERENCE: 210121.478C15
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nes 16; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
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                              212 GTCCTCCACTTTCACA 227
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   GTCCTCCACTTTCACA 428
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Retter, Marc
Mannion, Jane
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Carter, Darrick
Retter, Marc
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Lodes, Michael
Fanger, Gary
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                                                              Conservative
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                                                                         100.0%;
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                                                                                            7.0%;
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24;
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APPLICANT: Fan, Liqun

APPLICANT: Wang, Aijun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE

TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.478C15

CURRENT APPLICATION NUMBER: US/09/736,457

CURRENT FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 1864

SOFTWARE: FastSEQ for "1"

LENGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 1
SOFTWARE: FastSEQ for V
SEQ ID NO 46
LENGTH: 516
TYPE: DNA
ORGANISM: Homo sapien
US-09-702-705-46
                                                                                                            ; TYPE: DNA; Homo sapien; ORGANISM: Homo sapien US-09-736-457-46
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US-09-702-705-46
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                                                    Query Match
Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 46,
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C1.4
CURRENT PEPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
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                 212 GTCCTCCACTTTCACA 227
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413 GTCCTCCACTTTCACA 428
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Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
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Carter, Darrick
Retter, Marc
Mannion, Jane
Fan, Liqun
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Lodes, Michael A.
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Bangur, Chaitanya
Lodes, Michael A.
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Pred. No.
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Pred. No.
                                                       Mismatches
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US-09-702-705-794/c

Sequence

794,

Application US/09702705

RESULT 14

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                                                                                                          ; LENGTH: 970
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-794
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US-09-736-457-794/c
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; ORGANISM: Homo sapiens
US-09-702-705-794
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SEQ ID NO 794
LENGTH: 970
                                                   Query Match 7.0%; Score 16; Best Local Similarity 100.0%; Pred. No. Matches 16; Conservative 0; Mismatc
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Best Local Similarity
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                                                                                                                                                                                                        APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DATE: 2000-12-13
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CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
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                  212 GTCCTCCACTTTCACA 227
223
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GICCICCACTITCACA 208
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Vedvick, Tom
Carter, Darrick
Retter, Marc
Mannion, Jane
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Vedvick, Tom
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Bangur, Chaitanya
Lodes, Michael A.
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Lodes, Michael A.
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ır, Chaitanya S.
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US-09-205-258-67/c
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GENERAL INFORMATION:
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EARLIER FILING DATE: 1998-06-04
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TITLE OF INVENTION: 207 Human Secreted Proteins
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APPLICATION NUMBER: 60/049,374
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,915
FILING DATE: 1997-06-06
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                              APPLICATION NUMBER: 60/048,917
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,949
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/049,373
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,875
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/048,970 FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,974 FILING DATE: 1997-06-06
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NUMBER: 60/048,883

APPLICATION NUMBER: 60/048,898

APPLICATION I

DATE: 1997-06-06

NUMBER: 60/048,897 1997-06-06

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US-09-453-702B-188/c
Sequence 188, Application US/09453702B
Parent No. 6365723
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 1227
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EARLIER APPLICATION NUMBER: 60/070,923
EARLIER FILING DATE: 1997-12-18
EARLIER APPLICATION NUMBER: 60/092,921
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EARLIER APPLICATION NUMBER: 60/094,657
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LOCATION: (668)
OTHER INFORMATION:
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LOCATION: (745)
OTHER INFORMATION:
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TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: (1113)
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LOCATION: (1088)
OTHER INFORMATION: n
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LOCATION: (1015)
OTHER INFORMATION: n
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           Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences
NUMBER OF SEQUENCES: 265
                                                                                                APPLICANT: Blattner, Frederick R.
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                              501 TCACCTCCGTCCCTCC 486
                                                                                                                                                                                                                                                    190 TCACCTCCGTCCCTCC 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 60/048,877
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,963
FILING DATE: 1997-06-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/048,962
                                                                                                                                                                                                                                                                                        l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              (1110)
                                                                                                                                                                                                                                                                                     7.0%; Score 16; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
                                  Periu,
Plunkett, ou,
Th. Rod
                                                                       Burland, Valerie
Perna, Nicole T.
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                                                                                                                                                                                                                                                                                                                                                                                                                            equals a,t,g,
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                                                       Guy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a, t, g,
                                                                                                                                                                                                                                                                                        Mismatches
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                            of E. coli 0157
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TOPOLOGY: linear;
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MOLECULE TYPE: DNA (genomic);
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SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-453-702B-188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
APPLICATION 435
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/211,15(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Willem
APPLICANT: Sonder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 188: SEQUENCE CHARACTERISTICS:
                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Batentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,617
                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Vector vaccines of r
TITLE OF INVENTION: Feline herpesviruses
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           STATE: Maryland
                                                                                                                                                                                                                                                                                                                              CITY: Rockville
                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Akzo No. 6521236el
STREET: 1330 Piccard Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                   20850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Quarles & Brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                           Willemse, Martha Jacoba
Sondermeijer, Paulus Jacobus Antonius
VENTION: Vector vaccines of recombinant
                                                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
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                                         08/211,150
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SEQUENCE CHARACTERISTICS:

ENGTH:

6154 base pairs

nucleic acid

TELECOMMUNICATION INFORMATION:

258-5200

TELEPHONE:

ATTORNEY/AGENT INFORMATION:

NAME: Gormley, Mary E. REGISTRATION NUMBER: 3

34,409

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US-09-177-249-6
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Patent No. 6229064
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
APPLICANT: Goldberg, Robert B.
APPLICANT: The Regents of the University of California TITLE OF INVENTION: Nucleic Acids That Control Seed and TITLE OF INVENTION: Development in Plants
FILE REFERENCE: 023070-086120US
CURRENT APPLICATION NUMBER: US/09/177,249
CURRENT APPLICATION NUMBER: US/09/177,249
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: US 09/071,838
EARLIER FILING DATE: 1998-05-01
                                                                                                                                                                        APPLICANT: Ohad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramin
APPLICANT: Margossian, Linda
                                                                                                                                                                                                                                                              ENERAL
                                                                                                                                                             APPLICANT: Harada, John
                                                                                                                                                                                                                                           ENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN: G2620
[MMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: FEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
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LOCATION: complement (4256..4897)
OTHER INFORMATION: /label= ORF-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: 127..1281
OTHER INFORMATION:
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LOCATION: complement (5138..6142)
OTHER INFORMATION: /label= ORF-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 3055..3357
OTHER INFORMATION: /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 1460..3058
OTHER INFORMATION: /label= ORF-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                   3256 CTACCGATTTTCTATT 3241
                                                                                                                                                                                                                                                                                                                                                                                                                   105 CTACCGATTTCTATT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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3505..3963
3507... /label= ORF-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.0%; Score 16;
100.0%; Pred. No.
Live 0; Mismatcl
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26;
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                                                                                                           and Fruit
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RESULT 18
US-09-922-445-1
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Patent No. 6528268
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver.
SEQ ID NO 6
LENGTH: 7015
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: GG126US
CURRENT APPLICATION NUMBER: US/09/922,445
CURRENT FILING DATE: 2001-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Andersson, APPLICANT: Berglund,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (3)..(7013)
OTHER INFORMATION: fertilization-independent endosperm 1 (FIE1)
OTHER INFORMATION: SET/polycomb gene genomic sequence reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)..(7014)
OTHER INFORMATION: fertilization-independent
OTHER INFORMATION: SET/polycomb gene genomic
                                                                                                                                                                                                                                                   OTHER INFORMATION: nucleotide OTHER INFORMATION: A or G
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (2)..(7015)
OTHER INFORMATION: fertilization-independent
OTHER INFORMATION: SET/polycomb gene genomic
                                                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                    LOCATION: (1)..(26156)
OTHER INFORMATION:
NAME/KEY: misc_feature
LOCATION: (24801)..(24801)
                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
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                             LOCATION: (26402).
OTHER INFORMATION:
                                                                                 LOCATION: (26253).
                                                                                                                                  LOCATION: (26157)..(26252)
OTHER INFORMATION:
                                                                                                                                                                  NAME/KEY: exon
                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (24941)..(24941)
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                 NAME/KEY:
                                                                  NAME/KEY:
                                                                                                                    NAME/KEY: Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
mes 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1319 ATTTTCTATTTCTTGC 1334
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                                                                 exon
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                                                                                                  (26253)..(26401)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reneland, Rikard H. Adam, Gail I. R.
(26544) . . (27024)
                                                 (26402) . . (26543)
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                                                                                                                                                                                 nucleotide
T or C
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                                                                                                                                                                                                   a single nucleotide polymorphism
                                                                                                                                                                                                                                                                      a single nucleotide polymorphism which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
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sequence reading frame
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can

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can be

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US-09-922-445-1
Query Match 7.0%; Score 16; DB 4; Best Local Similarity 100.0%; Pred. No. 28; Matches 16; Conservative 0; Mismatches
                                                                                      NAME/KEY: exon
LOCATION: (3842)..(38653)
OTHER INFORMATION:
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank/AC004923
DATABASE ENTRY DATE: 1999-12-21
RELEVANT RESIDUES: (1)..(38653)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (27645)...(27645)
OTHER INFORMATION: mucleotide 27645 is a single nucleotide polymorphism which
OTHER INFORMATION: C or G
                                                                                                                                                                                                                         NAME/KEY: Intron
LOCATION: (36524).
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       JAME/KEY: Intron
LOCATION: (34589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (32614)..(326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DTHER INFORMATION: nucleotide 32163 is a single nucleotide polymorphism which can DTHER INFORMATION: A or C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WAME/KEY: exon
LOCATION: (30895)..(31027)
OTHER INFORMATION:
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LOCATION: (27179)..(30519)
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OCATION: (32163)..(32)
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OCATION: (31028)..(31747)
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THER INFORMATION:
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OCATION: (33598)..(34314)
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THER INFORMATION:
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THER INFORMATION:
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                                    Length 38653;
   Indels
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US-09-539-333D-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patent.pm
SEQ ID NO 1
LENGTH: 319608
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APPLICANT: Blumen:
APPLICANT: Chumak
APPLICANT: Bougue
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PRIOR FILING DATE: 1999-10-12
NUMBER OF SEQ ID NOS: 231
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PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: US 60/145,915
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US 60/146,453
PRIOR FILING DATE: 1999-07-29
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APPLICANT: Essioux, Laurent
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
FILE REFERENCE: GENSET.047AUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 1999-04-30
                                                                                                                                                                                                                              FEATURE.
NAME/KEY: exon
'CATION: 18778...18862
'CATION: PARTION: exon
NAME/KEY: exon
LOCATION: 29967..30282
OTHER INFORMATION: exon E g35018 gene
                                                                          NAME/KEY: exon
LOCATION: 29388..29502
OTHER INFORMATION: exon
                                                                                                                                                                            NAME/KEY: exon
LOCATION: 25593..25740
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LOCATION: 1108..1289
OTHER INFORMATION: exon
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LOCATION: 31..1107
OTHER_INFORMATION: 5'regulatory region g35018
                                                                                                                                                           LOCATION: 25593..25740
OTHER INFORMATION: exon
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LOCATION: 14877
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                                                              FEATURE:
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OTHER INFORMATION: exon
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FILING DATE: 1999-07-29
APPLICATION NUMBER: US 60/162,288
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Bougueleret, Lydie
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FEATURE:
NAME/KEY: exon
64666..64812
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LOCATION: 231272..231412
OTHER INFORMATION: exon
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LOCATION: 230408..230721
OTHER INFORMATION: exon P
FEATURE:
NAME/KEY: exon
LOCATION: 231787..231880
OTHER INFORMATION: exon O2 complement g34872 gene
                                                                                                                                                                                             NAME/KEY: exon
LOCATION: 229647..229742
OTHER INFORMATION: exon
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TWEORMATION: exon Q1
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NAME/KEY: exon
LOCATION: 65505..65853
OTHER INFORMATION: exon G
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LOCATION: 215819..215975
DTHER INFORMATION: exon I
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LOCATION: 216836..216915
OTHER INFORMATION: exon V g35030 gene
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LOCATION: 94124..94964
OTHER INFORMATION: exon g35017
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LOCATION: 216661..217061
OTHER INFORMATION: exon
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JOCATION: 216661..216952
JTHER INFORMATION: exon Qbis complement g34872 gene
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LOCATION: 213818..2158
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JOCATION: 215702..215746
JTHER INFORMATION: exon U
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JOCATION: 214676..214793
DTHER INFORMATION: exon
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LOCATION: 65854..67854
OTHER_INFORMATION: 3'regulatory region g35018 gene
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OCATION: 215819..215941
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OCATION: 201188..201234
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Best Local Similarity
Matches 16; Conserva
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NAME/KEY:
LOCATION:
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LOCATION: 241686..243685
OTHER INFORMATION: 5'regulatory region g34872
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NAME/KEY: exon
LOCATION: 239719..239853
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NAME/KEY: exon
*OCATION: 239719..239807
*TOWNTION: exon N2
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LOCATION: 231870..231879
OTHER INFORMATION: exon O1
                                                                                                                                                      OTHER INFORMATION: 3'regulatory region g34665 gene
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon 1
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LOCATION: 240528...2
OTHER INFORMATION:
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LOCATION: 240528..240824
OTHER INFORMATION: exon M862 complement
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LOCATION: 240528..240644
OTHER INFORMATION: exon MS2
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LOCATION: 237406..237428
OTHER INFORMATION: exon Nbis
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LOCATION: 290652..292652
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LOCATION: 240528..240596
OTHER INFORMATION: exon M1090 complement g34872 gene
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LOCATION: 240528..240569
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LOCATION: 234174..234321
OTHER INFORMATION: exon O
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OTHER INFORMATION: exon M1069
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292653..292841
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SOFTWARE:
SEQ ID NO 1
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APPLICANT: Chumakov, 11ya
APPLICANT: Bougueleret, Lydie
APPLICANT: Essioux, Laurent
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENE,
FILE REFERENCE: 53.US15.CIP
CURRENT APPLICATION NUMBER: US/09/679,409
CURRENT FILING DATE: 2000-10-03
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PRIOR APPLICATION NUMBER:
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PRIOR FILING DATE: 2000-03-03
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: 199122..201122
OTHER: INFORMATION: 5'regulatory region
                                                                                                                                                                                                                                                                                                                        NAME/KEY: exon
LOCATION: 238715..238919
OTHER INFORMATION: exon V3
                                                                                                                                                                                                                NAME/KEY: exon
LOCATION: 240440..241153
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OTHER INFORMATION: exon V4
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OTHER INFORMATION: exon S2
OTHER INFORMATION: exon NAME/KEY: misc_feature
                                                                              LOCATION: 244353..244561
OTHER INFORMATION: exon
                                                                                                                                          OTHER INFORMATION: exon
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OTHER INFORMATION: exon V1
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OTHER INFORMATION: exon V2
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LOCATION: 216836..216994
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LOCATION: 201123..201234
                                                             NAME/KEY: exon
                                                                                                                                                                                                     OTHER INFORMATION: exon W2
                                                                                                                                                                                                                                                                   OTHER INFORMATION: exon W
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5. 6555316
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NAME/KEY: allele
LOCATION: 160876
OTHER INFORMATION: 99-24634-108 : pc
NAME/KEY: allele
LOCATION: 168974
OTHER INFORMATION: 99-7652-162 : pc.
NAME/KEY: allele
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NAME/KEY: allele
LOCATION: 202679
OTHER INFORMATION: 8
NAME/KEY: allele
LOCATION: 203378
OTHER INFORMATION: 8
NAME/KEY: allele
LOCATION: 204138
NAME/KEY: allele
LOCATION: 204138
                                                                              NAME/KEY: allele
LOCATION: 206064
OTHER INFORMATION: 8
NAME/KEY: allele
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OTHER INFORMATION: 9
NAME/KEY: allele
LOCATION: 173358
OTHER INFORMATION: 9
NAME/KEY: allele
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OTHER INFORMATION: 99-27935-193 : polymorphic b
NAME/KEY: allele
LOCATION: 65485
OTHER INFORMATION: 8-128-33 : polymorphic base
                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 205206
OTHER INFORMATION: 8-295-248
                                                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: 204934
OTHER INFORMATION:
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LOCATION: 200778
OTHER INFORMATION: 8-303-235 :
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OTHER INFORMATION: 99-5919-215 : polymorphic base A o NAME/KEY: allele
LOCATION: 197163
OTHER INFORMATION: 99-24658-410 : polymorphic base A
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LOCATION: 160640
OTHER INFORMATION: 99-24639-163 : polymorphic base A or
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LOCATION: 95396
COTHER INFORMATION: 99-31960-363 : polymorphic base A or
NAME/KEY: allele
LOCATION: 107281
COTHER INFORMATION: 99-24656-260 : polymorphic base A or
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NAME/KEY: allele
LOCATION: 8316
OTHER INFORMATION: 99-27943-150 : polymorphic base G
                                                 LOCATION: 206545
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 204605
OTHER INFORMATION: 8-252-190
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 OTHER INFORMATION: 8-251-322
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                                                                                             RESULT 21
                                    Sequence 254, Application US/09221017B Patent No. 6444799
GENERAL INFORMATION:
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Best Local
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OTHER INFORMATION: 8
NAME/KEY: allele
LOCATION: 210463
OTHER INFORMATION: 8
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LOCATION: 209123
OTHER INFORMATION:
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OTHER INFORMATION: 8-278-289
NAME/KEY: allele
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OTHER INFORMATION:
NAME/KEY: allele
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OTHER INFORMATION:
NAME/KEY: allele
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OTHER INFORMATION: 8-285-319
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: allele
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LOCATION: 210964
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LOCATION: 210879
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 208285
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APPLICANT: ROSS, BruTITLE OF INVENTION: NUMBER OF SEQUENCES:
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Pred. No.
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Query Match
Best Local Similarity
Matches 15; Conserve
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US-09-252-991A-51/c
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US-09-221-017B-254
                                                                                                Sequence 51, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
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LENGTH: 920 base pairs
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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OPERATING SYSTEM: Windows
OPERWARE: FASTERO for Windows Version 2.0b
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TELEPHONE: 650-494-0792
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REGISTRATION NUMBER:
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Pred. No.
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                                                                                                                                                                                                                                                                                       Length 920;
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
FEATURE:
FEATURE:
NAME/KEY: unsure
LOCATION: (102)
OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1108:
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/085,598
APPLICATION NUMBER: 60/085,598
APPLICATION NUMBER: 60/051571
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE,DOCKET NUMBER: 6TC-012
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02354
COMPUTER READABLE FORM:
                                            FEATURE:
                                                                                   ORIGINAL SOURCE:
                                                                                                      TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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NAME/KEY: misc feature LOCATION: (B) LOCATION 1...975
                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                  ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                           TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: CD/ROM ISO9660
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                                                                                                                                                                                                                             ENGTH: 975 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and David Bush
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84;
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APPLICANT: Martin, Robert R.
APPLICANT: Mathews, Helena
APPLICANT: Mathews, Helena
APPLICANT: Keller, Karen
APPLICANT: Keller, Karen
APPLICANT: Wegner, Ry
TITLE OF INVENTION: Development of Resistance to Ras
TITLE OF INVENTION: Development of Virus
TITLE OF INVENTION: Dusarf Virus
FILE REFERENCE: 4257-0024.31
CURRENT APPLICATION NUMBER: US/09/784,508
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/737,719
PRIOR APPLICATION NUMBER: US 60/171,018
PRIOR FILING DATE: 1909-01-25
NUMBER OF SEQ ID NOS: 16
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US-09-784-508-16
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Patent No. 6548742
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SOFTWARE: 1
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Best Local Similarity
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CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/737,719
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 60/171,018
PRIOR FILING DATE: 1999-01-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kellogg, Jill A.
APPLICANT: Wagner, Ry
TITLE OF INVENTION: Development of Resistance to Raspberry
TITLE OF INVENTION: Bushy Dwarf Virus
FILE REFERENCE: 4257-0024-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mathews, Hearn
APPLICANT: Mathews, Hearn
APPLICANT: Keller, Karen
Trant: Keller, Karen
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TYPE: DNA
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                 FastSEQ for Windows Version 4.0
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100.0%;
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Pred. No.
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Pred. No.
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; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2461
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US-09-697-367-7/c
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                                                                                                                                                                                                                        FILE REFERENCE: BB1166 US NA
CURRENT APPLICATION NUMBER: US/09/697,367
CURRENT TILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/084,529
PRIOR FILING DATE: 1998-MAY-07
PRIOR PPLICATION NUMBER: PCT/US99/09865
PRIOR FILING DATE: 1999-MAY-06
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                           SOFTWARE:
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application US/09697367 Patent No. 6323015
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Best Local Similarity
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tarczynski, Mitchell
FITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                  LENGTH: 1611
TYPE: DNA
ORGANISM: Zea mays
                                                                                    NAME/KEY: unsure LOCATION: (14)
                                  NAME/KEY:
                                                                       VAME/KEY:
                                                   OCATION:
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les 15; Conservative
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                                                   : unsure
: (1424)
                                                                                                                                                                                                             Microsoft Office 97
                unsure
(1469)
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unsure
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Caimi, Perry G.
Weng, Zude
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Pred. No.
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85;
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Query Match
Best Local Similarity
"`~ hes 15; Conserv?
                                                                      US-08-936-165A-224
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Best Local :
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                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/027
APPLICATION UNMBER: 50/027
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (1515)
NAME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/936,165A FILING DATE: 24-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                  TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                TELEFAX: 610-270-5090
                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                         ENGTH:
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                                                                                                                                         1886 base pairs
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosenberg, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reichard, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pratt, Julie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Knowles, David
Lonetto, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burnham, Martin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Black, Michael
                                                                                                linear
                                                                                                                                                                                                                610-270-4478
                                                                                  Genomic DNA
                                                                                                           single
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Polypeptides and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          John
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Richard
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                         Score 15; Pred. No.
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                          DB 4;
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86;
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US-08-934-494-5/c
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US-08-933-821-16/c
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Patent No. 6030831
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Patent No. 5972338
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Gurney
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                           APPLICANT: Gurney, Austin
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MEDIUM TYPE: 3.5 inc
                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                             NUMBER OF SEQUENCES:
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                                                                     STREET: 1 DNA "",
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                              6.6%;
Local Similarity 100.0%;
nes 15; Conservativo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 2042 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                           DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                   640 GATTTTCTATTTCTT 626
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                                                         94080
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                                                                                                                                           Genentech, Inc.
                                                                                                                                                                             Tie Ligands
15
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Query Match
Best Local Similarity
Watches 15; Conserva
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                                                                              US-08-960-507-16
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Patent No. 6057435
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
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                                                                                                       LENGTH: 2042 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
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SOFTWARE: WinPatin
                                                                                            STRANDEDNESS:
TOPOLOGY: Li
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STRANDEDNESS: Single
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             6.6%; Score 15; DB ilarity 100.0%; Pred. No. 86; Conservative 0; Mismatches
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                                           Length 2042;
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               Indels
               0;
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110 GATTTTCTATTTCTT 124

640 GATTTTCTATTTCTT 626

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Sequence 5, Application US/09143707
Patent No. 6348350
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 15
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US-09-143-068-5/c
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Matches
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APPLICANT: Goddard, Audrey
APPLICANT: Godwaki, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth
APPLICANT: Williams, Mickey
TITLE OF INVENTION: Tie Ligand Homologues
NUMBER OF SEQUENCES: 17
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/143,068
FILING DATE: 28-Aug-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 2042 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: South San Francisco
STATE: California
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                   ADDRESSEE:
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15; Conserv
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E: Genentech, Inc.
1 DNA Way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2042 base pairs
                                                                                                            SEQ ID NO 5
LENGTH: 2042
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09202089 Patent No. 6348351
                                                    Best
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                                                                  Query Match
                                                                                                                                                                                                                             APPLICANT: Williams, Mickey
TITLE OF INVENTION: Tie Ligand Homologues
FILE REFERENCE: P1078P2(e)
CURRENT APPLICATION NUMBER: US/09/202,089
CURRENT FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: PCT/US98/19094
PRIOR FILING DATE: 1998-09-14
                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 08/934,494 PRIOR FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/143,707
APPLICATION NUMBER: US/09/143,707
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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STRANDEDNESS: Single
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                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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   110 GATTTTCTATTTCTT 124
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                                   l Similarity
15; Conserv
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Hillan, Kenneth
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Godowski, Paul J.
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                                  6.6%; Score 15;
100.0%; Pred. No.
tive 0; Mismatc
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100.0%; Pred. No. 86;
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                                                 DB 4;
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RESULT 35
US-09-136-828-16/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 2042 base pairs
TYPE: Nucleic Acid
STRANDENNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0%; F
                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/09332928A Patent No. 6368853 GENERAL INFORMATION:
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Patent No. 6350450
GENERAL INFORMATION:
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NAME: Dreger, Ginger R.

REGISTRATION NUMBER: 3,055
REFERENCE/DOCKET NUMBER: P113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEPAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
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APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WinPatin (Ge CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 1
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/136,828
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STATE: California
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           ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                               Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                          APPLICANT: Godowski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 GATTTTCTATTTCTT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 640 GATTTTCTATTTCTT 626
                                                                                                                                                                    STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
APPLICATION NUMBER: US/09/332,928A
                                                                                                                                                      COUNTRY: USA
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L00.0%; Pred. No.
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86;
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APPLICANT:

Botstein, David Goddard, Audrey

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APPLICANT

Roy, Margaret

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-511-133-5
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                                                                                                                          RESULT 38
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                                                                                                         US-09-136-801-16/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
FILE REFERENCE: p1078R1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09511133
Patent No. 6372491
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TELEPAX: 650/952-9881
INFORMATION FOR SBO ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 2042 base pairs
TYPE: Nucleic Acid
STRANDENNESS: Single
TOPOLOGY: Linear
                                                  Sequence 16, Applicat Patent No. 6413770 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 5
LENGTH: 2042
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CURRENT FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: US 09/143,707
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: US 60/059,352
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
NUMBER OF SEQ ID NOS: 15
 APPLICANT:
                  APPLICANT:
                                                                                                                                                                                                                                                  Local Similarity nes 15; Conserv
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APPLICATION NUMBER: 08/933,821
FILING DATE: <Unknown>
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                                                                                                                                                                                                110 GATTTTCTATTTCTT 124
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                                                                    s, Application US/09136801
6413770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-Jun-1999
CLASSIFICATION: <Unknown
Gurney, Austin
Hillan, Kenneth
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                                   Godowski, Paul
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100.0%; Pred. No. 86;
                                                                                                                                                                                                                                                                     6.6%; Score 15; DB 4; Length 2042; L00.0%; Pred. No. 86;
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PPLICANT:

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Matches 15; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: Tie Ligand Homologues
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1 DNA "", CITY: South San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2042 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                              APPLICATION NUMBER: FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                       1 DNA Way
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 08/933,821
                                                                   US/09/332,929
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Sequence 5, Application US/09511631
Patent No. 6455496
GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Austin L.
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
FITTLE OF INVENTION: Tie Ligands
FILE REFERENCE: P1078R1D1
CURRENT APPLICATION NUMBER: US/09/511,631
CURRENT FILING DATE: 2000-02-33
PRIOR APPLICATION NUMBER: US 09/143,707
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: US 60/059,352
PRIOR FILING DATE: 1997-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SOFTWARE: FastSEQ for Windows Version
; SEQ ID NO 5
; LENGTH: 2042
; TYPE: DNA
; ORGANISM: Homo sapiens .
US-09-690-169-5
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                                                                                                                                                                                                                                                                            US-09-511-631-5/c
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Best Local Similarity 100.0%;
Matches 15; Conservative
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APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Gurney, Austin
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Patent No. 642621
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SEQUENCE CHARACTERISTICS:
LENGTH: 2042 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/143,707
PRIOR FILING DATE: 1998-08-28
PRIOR APPLICATION NUMBER: 60/059,352
PRIOR FILING DATE: 1997-09-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: GENENT. 58A2D2
CURRENT APPLICATION NUMBER: US/09/690,169
CURRENT FILING DATE: 2001-09-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEPHONE: 650/225-3216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
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nes 15; Conserv
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STRANDEDNESS: Single
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Pred. No.
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RESULT 43
US-09-630-189-5/c
; Sequence 5, Application US/09690189
; Patent No. 6521234
; GENERAL INFORMATION:
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US-09-333-075-16/c
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                                                                                                                                                                                                                                                               TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
LENGTH: 2042 base pairs
TYPE: Nucleic Acid
STRANDENESS: Single
                                                                                                                                                                      Query Match 6.6%; Score 15; Best Local Similarity 100.0%; Pred. No. Matches 15; Conservative 0; Mismatc
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LENGTH: 2042
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Best Local Similarity
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                            NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
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APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
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STATE: California
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                                                                                                             640 GATTTTCTATTTCTT 626
                                                                                                                                          110 GATTTTCTATTTCTT 124
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86;
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RESULT 45
US-09-33-077-16/c
; Sequence 16, Application US/09333077
; Patent No. 6586397
; GENERAL INFORMATION:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-690-189-5
                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-202-088A-16
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Best Local Similarity
Matches 15; Conserv
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LENGTH: 2042
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CURRENT APPLICATION NUMBER: US/09/202,088A
CURRENT FILING DATE: 1998-12-08
PRIOR APPLICATION NUMBER: PCT/US98/19093
PRIOR FILING DATE: 1998-09-14
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION
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Best Local Similarity
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/690,189
CURRENT FILING DATE: 2000-10-16
PRIOR APPLICATION NUMBER: US 09/143,707
PRIOR FILING DATE: 1998-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Goddard, Audrey APPLICANT: Godowski, Paul
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APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Tumas, Daniel
APPLICANT: Schwall, Ralph
TITLE OF INVENTION: TIE LIGAND HOMOLOGUES
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           APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Tie Ligands
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
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Hillan, Kenneth
Botstein
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Ferrara, Napoleone
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1 DNA Way
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100.0%; Pred. No.
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Pred. No.
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86;
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CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: NIM PC compatable
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER STATE:
COMPUTER STA
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Result
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Maximum DB
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                                                                                                                                                                                                                                                                               Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq
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1: /cgn2 6/ptodata/1/pubpna/US07 PUBCOMB.seq:*

2: /cgn2 6/ptodata/1/pubpna/PCT NEW PUB.seq:*

3: /cgn2 6/ptodata/1/pubpna/US06 NEW PUB.seq:*

4: /cgn2 6/ptodata/1/pubpna/US07 NEW PUB.seq:*

5: /cgn2 6/ptodata/1/pubpna/US07 NEW PUB.seq:*

6: /cgn2 6/ptodata/1/pubpna/US07 NEW PUB.seq:*

6: /cgn2 6/ptodata/1/pubpna/US08 NEW PUB.seq:*

7: /cgn2 6/ptodata/1/pubpna/US08 PUBCOMB.seq:*

8: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

9: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

10: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

11: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

12: /cgn2 6/ptodata/1/pubpna/US09 PUBCOMB.seq:*

13: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*

14: /cgn2 6/ptodata/1/pubpna/US09 NEW PUB.seq:*

15: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*

16: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*

17: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*

18: /cgn2 6/ptodata/1/pubpna/US10 NEW PUB.seq:*
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US-10-027-632-195212
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US-10-027-632-199347
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US-10-027-632-3199347
US-10-027-632-3109348
US-10-027-632-3109349
US-10-428-487-11
US-10-428-535A-25921
US-10-242-535A-25921
US-10-027-632-310795
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            Sequence 12566, A
Sequence 302898,
Sequence 302898,
Sequence 195212,
Sequence 195212,
Sequence 199347,
Sequence 199346,
Sequence 199346,
Sequence 199346,
Sequence 199347,
Sequence 119346,
Sequence 219346,
Sequence 219347,
Sequence 310795,
Sequence 310795,
Sequence 310795,
11, Appl
18845, A
23845, A
25921, A
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US-10-154-884B-2901	US-10-057-475B-2901		US-10-040-862-3452	US-10-154-884B-3452	US-10-057-475B-3452	US-09-796-692-3452	US-10-040-739-1242	US-10-033-528-1718	US-10-099-926-1718	-09-920	US-10-242-535A-29962	US-10-216-441-3	US-09-818-656A-3	-319	US-09-764-877-3198	-10-242-515-	-09-76	US-10-074-045-70	-09-764-891-	-10-037-270-	US-10-117-722-916	-10-191-997-	US-09-815-242-7429	US-10-027-632-149574	US-10-027-632-149573	US-10-027-632-149574	-027-	-09-818-656A-9	US-09-818-656A-94
æ	e 2901,	e 2901,	e 3452,	3452,	e 3452,	3452,	1242,	e 1718,	1718,	•	2996	3,	3, 1	Sequence 3198, Ap	3198	319	3194	70,	7123	916,	e 916,	e 130,	Sequence 7429, Ap	Sequence 149574,		O	æ	95,	Sequence 94, Appl

ALIGNMENTS

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US-09-918-995-12566/c

Sequence 12565, Application US/09918995

Publication No. US20030073623A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES

FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995

CURRENT APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR APPLICATION NUMBER: US/09/235,076

PRIOR FILING DATE: 1999-01-20

NUMBER OF SEQ ID NOS: 38054
                                                                                                                                            ; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(476)
; OTHER INFORMATION: n = A,T,C
US-09-918-995-12566
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                                                                      Query Match
Best Local S
Matches 18
                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 12566
                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                              LENGTH: 476
110
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                                                                      l Similarity
18; Conserv
                   ATTTTTGATGGCCTTAAG 55
ATTTTTGATGGCCTTAAG
                                                                  7.9%; So lilarity 100.0%; I conservative 0;
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k; Pred. No. 14;
0; Mismatches
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                                                                      Gaps
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RESULT 2 US-10-027-632-302898/c ; Sequence 302898, Application US/10027632 ; Publication No. US20030204075A9

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RESULT 3
US-10-027-632-302898/c
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 302898, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
          Matches
                         Query Match
Best Local
                                                                                                                                                                        SEQ ID NO 302898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
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TYPE: DNA
ORGANISM: Human
                                                                                                          ORGANISM: Human
                                                                                                                                 TYPE: DNA
                                                                                                                                                  ENGTH:
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FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
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        18; Conservative
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                             Similarity
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7.5%; PI.
100.0%; PI.
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      7.9%; Score 18; DB
100.0%; Pred. No. 14;
ive 0; Mismatches
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                         DB 14;
14;
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; ORGANISM: Human
US-10-027-632-195212
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US-10-027-632-195212
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SOFTWARE: FastSEQ for
SEQ ID NO 195212
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                                                                 PRIOR FILING DATE: 1999-09-28
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                                                                                       PRIOR APPLICATION NUMBER: US 60/156,358
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                         APPLICATION NUMBER: US 60/146,002 FILING DATE: 1999-08-09
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PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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                                                                                                                                                                             APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
                                                  PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-11-23
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US-10-027-632-199346/c ; Sequence 199346, Application US/10027632 ; Publication No. US20030204075A9
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SEQ ID NO 195212
LENGTH: 481
TYPE: DNA
                                                                                                                                                                                  Sequence 199347, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome
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Matches
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              CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                                                                                                          APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 637
TYPE: DNA
ORGANISM: Human
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FILING DATE: 2000-04-20
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                                                                                                                                                                                                                                                                                                                               465
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Pred. No
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Pred. No.
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US-10-027-632-199346/c
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US-10-027-632-199347
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SEQ ID NO 199346
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GENERAL INFORMATION:
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                                                                                         Query Match
Best Local Similarity
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 108827.129
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                                                                                                                                                                                    TYPE: DNA
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465
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                                    ATAAAGCACTCAATTTCT 29
ATAAAGCACTCAATTTCT 448
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                                                                                     100.0%;
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Pred. No.
                                                                                           Score 18;
Pred. No.
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                                                                                                            DB 14; Length 637;
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RESULT 9 US-10-027-632-199347/c Sequence 199347, Application US/10027632 GENERAL INFORMATION:

APPLICANT: Wang, David G.

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RESULT 11
US-09-918-995-18845/c
; Sequence 18845, Application US/09918995
; Publication No. US20030073623A1
. GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA; ORGANISM: Homo sapiens
US-10-428-487-11
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR TILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 2000-02-24
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Best Local Similarity
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Best Local Similarity 100.0%;
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APPLICANT: RESER, HANG-PETER
APPLICANT: GERBER, HANG-PETER
TITLE OF INVENTION: VEGF-MODULATED GENES AND METHODS EMPLOYING
FILE REFERENCE: 09800080-0103
CURRENT APPLICATION NUMBER: US/10/428,487
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: 09/815,153
PRIOR FILING DATE: 2001-03-21
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,201
PRIOR APPLICATION NUMBER: 60/191,201
PRIOR APPLICATION NUMBER: 60/191,201
PRIOR FILING DATE: 2000-03-22
NUMBER OF SEQ ID NOS: 84
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
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US-10-242-535A-23845
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CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILLING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILLING DATE: 2001-03-12
PRIOR FILLING DATE: 2001-03-12
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CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 18845
LENGTH: 378
                                                           Sequence 25921, Application US/10242535A Publication No. US20040013663A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.2 SEQ ID NO 23845
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Best Local :
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APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 58994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing
FILE REFERENCE: 4231/2005
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NAME/KEY: misc_feature

LOCADION: (1)...(378)

OTHER INFORMATION: n = A,T,C or
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CURRENT APPLICATION NUMBER: US/10/242,535A CURRENT FILING DATE: 2002-09-12

FILE REFERENCE: 4231/2005

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PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 25921
LENGTH: 450
                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome
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Sequence 310795, Application US/10027632
Publication No. US20030204075A9
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
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LOCATION: (291)...(291)
OTHER INFORMATION: n is a,
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LOCATION: (283)..(283)
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LOCATION: (197)..(197)
OR APPLICATION NUMBER: US 60/193,483
OR FILING DATE: 2000-03-29
OR APPLICATION NUMBER: US 60/185,218
OR FILING DATE: 2000-02-24
OR APPLICATION NUMBER: US 60/167,363
OR FILING DATE: 1999-11-23
OR APPLICATION NUMBER: US 60/156,358
OR APPLICATION NUMBER: US 60/156,358
OR APPLICATION NUMBER: US 60/146,002
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                                                                                                                                                                                                                                                               US-09-818-656A-94
APPLICANT: GONG, FRANGCHENG et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: INCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOO1191
CURRENT APPLICATION UNMBER: US/09/818,656A
CURRENT FILING DATE: 2000-03-28
NUMBER OF SEQ ID NOS: 103
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 94
                                                                                                                                                                                                Sequence 94, Application US/09818656A Patent No. US20020142381A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 310795
LENGTH: 581
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SEQ ID NO 310795
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GENERAL INFORMATION
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
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CURRENT FILING DATE: 2002-04-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-818-656A-94
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 601
; TYPE: DNA
; ORGANIZSM: Homo sapiens
US-09-818-656A-95
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 149573, Application US/10027632 Publication No. US20030204075A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequent No. Usection:
Patent No. Usection:
Patent INFORMATION:
Patent No. Usection
Pat
                                 SEQ ID NO 149573
LENGTH: 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Wang, David G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/818,656A CURRENT FILING DATE: 2000-03-28
                                                                                                                                                         PRIOR FILING DATE: 1999-08-09 NUMBER OF SEQ ID NOS: 325720
                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 601
TYPE: DNA
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mes 17; Conserva
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17; Conservative
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Pred. No.
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51;
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
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US-10-027-632-149573
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US-10-027-632-149573/c
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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PRIOR FILING DATE: 1999-11-23
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17; Conserv
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NUMBER: US 60/167,363
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Pred. No.
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Pred. No.
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GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
Trawick, John D.
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US-10-027-632-149574
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US-10-027-632-149573
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GENERAL INFORMATION:
APPLICANT: Wang, Da
                                                                                      Sequence 7429, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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Best Local :
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PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 149573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Identification and Mapping of Single Nucleotide TITLE OF INVENTION: Polymorphisms in the Human Genome FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2002-04-30 PRIOR APPLICATION NUMBER: US 60/218,006 PRIOR FILING DATE: 2000-07-12
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TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60/193,483 FILING DATE: 2000-03-29 APPLICATION NUMBER: US 60/185,218 FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 60/146,002
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17; Conserv
                   Zyskind, Judith W. Wall, Daniel
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Pred. No.
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52;
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Query Match
Best Local Similarity
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US-10-191-997-130
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US-09-815-242-7429
                                                                                                          ; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: NM_001752
US-10-191-997-130
                                                                                                                                                                                               SOFTWARE: PatentIn version 3.1
SEQ ID NO 130
LENCTH: 2279
TYPE: DNA
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APPLICANT: THOMPSON, Terry
TITLE OF INVENTION: Oligonucleotide-Containing Pharmacological Compositions And Their
FILE REFERENCE: 54800-5019
CURRENT APPLICATION NUMBER: US/10/191,997
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,820
PRIOR PLING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 132
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/21,078
PRIOR APPLICATION NUMBER: 60/2106,848
PRIOR APPLICATION NUMBER: 60/206,848
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APPLICANT: DALE,
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PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
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27 TCTACTCAGAAATTTTT 43
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17; Conserv
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DALE, Roderic M. K.
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Pred. No.
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53;
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Publication No.
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (103)..(1686)
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PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
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TITLE OF INVENTION: NO. US20030219744A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2BCIP
CURRENT APPLICATION NUMBER: 09/01/117,722
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: 09/620,312
PRIOR FILING DATE: 2000-07-19
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/552,317
                                                       APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Zhiwei
APPLICANT: Tillinghast, John
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CIP2B
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Zhang, Jie
Ren, Feiyan
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Yang, Yonghong
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o. US20030219744A1
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100.0%; Pred. No.
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PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: pt FL-genes Version 1.0
SEQ ID NO 916
LENGTH: 2318
TYPE: DNA
ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: CDS
LOCATION: (103)...(1686)
US-10-037-270-916
Query Match
Best Local Similarity
"her 17; Conserva
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; ORGANISM: Homo sapiens
US-09-764-891-7122
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                                                                                   ; ORGANISM: Homo sapiens 
US-10-074-045-70
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 7122
LENGTH: 6352
                                                                                                                                                                                                                                                                                                   Sequence 70, Application US/10074045 Publication No. US20030092102A1 GENERAL INFORMATION:
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Best Local
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Best Local
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ21C1
                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/074,045
CURRENT FILING DATE: 2002-02-14
                                                                                                                                                                                    Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 74
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC006
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                                                                                                                  LENGTH: 18657
TYPE: DNA
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00.0%; Pred. No.
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               Score 17; DB; Pred. No. 64, 0; Mismatches
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56;
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; SEQ ID NO 3194
LENGTH: 28313
; TYPE: DIA
; ORGANISN: Homo sapiens
US-09-764-877-3194
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US-09-764-877-3194/c
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                     SOFTWARE: Paten
SEQ ID NO 3194
LENGTH: 28313
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CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
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                                                                                                                 Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 4031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2002-09-13
ORGANISM: Homo sapiens
10-242-515-3194
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PRIOR FILING DATE: 2000-01-31
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                                                                                                                                                        APPLICATION NUMBER: 60/218,290 FILING DATE: 2000-07-14
                                                                                                                                                                                                                                   FILING DATE: 2000-07-26
APPLICATION NUMBER: 60/217,496
FILING DATE: 2000-07-11
                                                                                                                                                                                                                                                                                             FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/220,963
                                                                                                                                                                                                                                                                                                                              FILING DATE: 2000-07-11
APPLICATION NUMBER: 60/225,758
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17; Conserv
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Pred. No.
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3198
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US-09-764-877-3198/c
Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3198
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Publication No. US20040009488A1
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Best Local
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CURRENT FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 09/764,877
PRIOR FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
PRIOR APPLICATION NUMBER: 60/180,628
PRIOR APPLICATION NUMBER: 60/180,628
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CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
                                                                          PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-07-14
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TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PC005C1
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                                                                                              FILING DATE: 2000-08-14
APPLICATION NUMBER: 60/218,290
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                                                                                                                          ; TYPE: DNA; ORGANISM: Homo spaiens US-10-216-441-3
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US-10-216-441-3
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Patent No. US20020142381A1
GENERAL INFORMATION:
APPLICANT: GONG, Fangcheng et al.
TITLE OF INVENTION: ISOLATED HUWAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL001191
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APPLICANT: GONG, Fa:
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                                                                                        Query Match
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TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM.
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOO1191CON
CURRENT APPLICATION NUMBER: US/10/216,441
CURRENT FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: 09/818,656
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 4
SCOTTUBER OF SEQ ID NOS: 4
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SOFTWARE: FastSEQ for Windows Version 4.0
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                  TTTCTATTTCTTGCCTC 129
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RESULT 34

RESULT 36 US-10-099-926-1718/c ; Sequence 1718, Application US/10099926

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FILE REFERENCE: 210121.547
CURRENT APPLICATION NUMBER: US/09/920,300A
CURRENT FILING DATE: 2001-07-31
NUMBER OF SEQ ID NOS: 1789
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1718
LENGTH: 287
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Liew, C.C.

APPLICANT: Liew, C.C.

TITLE OF INVENTION: Compositions and Methods Relatiing to FILE REFERENCE: 4231/2005

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US/10/085,783

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR APPLICATION NUMBER: US 60/375,017

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28
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US-10-242-535A-29962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 29962, Application US/10242535A Publication No. US20040013663A1
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                                                                          Matches
                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: King, Gordon E.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jianghun
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 58994
                                                                                                                                                                    FEATURE:
NAME/KEY: misc feature
NAME/KEY: misc feature
LOCATION: 29, 215, 242, 257
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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134
                                    189 CTCACCTCCGTCCCTC 204
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16; Conserv
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Pred. No.
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Pred. No.
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                                                                          Mismatches
                                                                          DB 10; I
0. 1.7e+02;
ches 0;
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1.7e+02;
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RESULT 38
US-10-040-739-1242/c
; Sequence 1242, Application US/10040739
; Publication No. US20020173635A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                  ; NAME/KEY: misc_feature; LOCATION: 29, 215, 242, 257; OTHER INFORMATION: n = A,T,C or US-10-033-528-1718
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; LOCATION: 29, 215, 242, 257
; OTHER INFORMATION: n = A,T,C or G
US-10-099-926-1718
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1718
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TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C2
CURRENT APPLICATION NUMBER: US/10/099,926
CURRENT FILING DATE: 2002-03-17
NUMBER OF SEQ ID NOS: 1982
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1718
LENGTH: 287
                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547C1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: King, Gordon B.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
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                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.0%; Pnes 16; Conservative 0;
                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                     189 CTCACCTCCGTCCCTC 204
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Jiang, Yuqiu
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100.0%; Pred. No.
tive 0; Mismatc
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                        APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001206
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/190,479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy Disk

COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
REPLICATION NUMBER: US/10/040,739
PILING DATE: 07-Jan-2002
CLASSIFICATION - CURKNOWN>
PRIOR APPLICATION NUMBER: 09/036,520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                      APPLICATION NUMBER: 60/200,545
FILING DATE: 2000-04-27
APPLICATION NUMBER: 60/200,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 1242:
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REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
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Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTATAAAGCACTCAA 188
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TYPE: nucleic acid
STRANDEDNESS: double
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: (617) 87
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; Pred. No. 1.8e+02;
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FILING DATE: 2000-04-28
APPLICATION NUMBER: 60/200,779
FILING DATE: 2000-04-28

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NAME/KEY: unsure
LICATION: (356)
THER INFORMATION: n=A,T,C or
US-09-796-692-3452
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LENGTH: 422
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                                                                             Sequence 3452, Application US/10057475B Publication No. US20040002068A1
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                 -10-057-475B-3452/c
                                                 APPLICANT: Order, Nadia
APPLICANT: Carter, Lauren
APPLICANT: McNeill, Patricia Dianne
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-014402US
CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2002-01-22
                                                                                                                                                                                                          APPLICANT:
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SOFTWARE: FastSEQ for Windows Version
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
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LOCATION: (340)
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: (151)
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FILING DATE: 2000-05-01
APPLICATION NUMBER: 60/202,084
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FILING DATE: 2000-05-22
APPLICATION NUMBER: 60/218,950
FILING DATE: 2000-07-14
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APPLICATION NUMBER: 60/222,903
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16; Conserva
                                                                                                                                                                                                        Algate, Paul A.
Mannion, Jane
Clapper, Jonathan David
Wang, Aijun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.0%; Score 16;
.00.0%; Pred. No.
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hes 0;
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                                                                                                                          the Detection,
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                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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US-10-154-884B-3452/c
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NUMBER OF SEQ ID NOS: 10979
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Compositions and Methods for TITLE OF INVENTION: Hematological Malignancies FILE REFERENCE: 014058-013521US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
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TYPE: DNA
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NAME/KEY: misc_feature
LOCATION: (1)...(422)
OTHER INFORMATION: n = 9,
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                                                                                PAPPLICATION NUMBER: US 6
FILING DATE: 2000-05-04
APPLICATION STATES TO STAT
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FILING DATE: 2000-04-28
APPLICATION NUMBER: US 60/200,779
FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/200,779
FILING DATE: 2000-04-28
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APPLICATION NUMBER: US 60/218,950
FILING DATE: 2000-07-14
APPLICATION NUMBER: US 60/222,903
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   FILING DATE:
APPLICATION N
                                                                            APPLICATION NUMBER: US 60/218,950
                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/202,084
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/200,999
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Retter, Marc W.
Corixa Corporation
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: 2000-07-14
NUMBER: US 60/222,903
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                                                                                                                                                     60/206,201
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Pred. No.
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. 1.8e+02;
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Therapy

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; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(422)
; OTHER INFORMATION: n = 9, a
US-10-154-884B-3452
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                                                        ; SEQ ID NO 3452
; LENGTH: 422
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-040-862-3452/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3452, Application US/10040862 Publication No. US20030078396A1
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Best Local Similarity
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                                                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 09/796,692 PRIOR FILING DATE: 2001-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/040,862
CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Hematological Malignancies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: Retter, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/200,303
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PRIOR FILING DATE: 2000-04-27
NAME/KEY: unsure
LOCATION: (151)
OTHER INFORMATION: n=A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/200,779
FILING DATE: 2000-04-28
                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/223,378 FILING DATE: 2000-08-07
                                                                                                                                                                                                                                                                                                    FILING DATE: 2000-08-03
APPLICATION NUMBER: US 60/223,416
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/222,903
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 2000-05-22
APPLICATION NUMBER: US 60/218,950
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 60/206,201
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                                                                                                                                                                                                                                                                                     FILING DATE: 2000-08-04
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Retter, Marc
Corixa Corporation
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Pred. No.
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US-09-796-692-2901
; ORGANISM: Homo sapiens
US-09-796-692-2901
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                                                                NUMBER OF SEQ ID NOS:
SOFTWARE: FASTSEQ for
SEQ ID NO 2901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2901, Application US/09796692 Publication No. US20020198362A1
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Best Local
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APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
                                                                                                                       PRIOR APPLICATION NUMBER: 60/223,378 PRIOR FILING DATE: 2000-08-07
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PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
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PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
                                  LENGTH: 42
TYPE: DNA
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NAME/KEY: unsure
LOCATION: (356)
OTHER INFORMATION: n=A,T,C
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OTHER INFORMATION:
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OTHER INFORMATION: n=A,T,C or G
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LOCATION: (165)
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hes 16; Conservative
                                                                                                                                                                                                               APPLICATION NUMBER: 60/222,903
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/202,084 FILING DATE: 2000-05-04
                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                          APPLICATION
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/200,779
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/218,950
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                                                                                                                                                                                                                                                                                                                                                        NUMBER: 60/200,999
                                                                                         for Windows Version 3.0
                                                                                                          2000-08-07
)S: 9597
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Pred. No. 1.8e+0;
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Query Match

7.0%;

Score 16;

DB 10;

Length 427;

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RESULT 45
US-10-154-884B-2901
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CURRENT APPLICATION NUMBER: US/10/057,475B
CURRENT FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,094
PRIOR APPLICATION NUMBER: US 60/200,094
PRIOR APPLICATION NUMBER: US 60/200,084
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-04
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; ORGANISM: Homo sapiens
US-10-057-475B-2901
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US-10-057-475B-2901
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                                                           Sequence 2901, Application US/10154884B Publication No. US20040005561A1 GENERAL INFORMATION:
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Best Local
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Publication No.
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APPLICANT:
APPLICANT:
                 APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 10979
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Carter, Lauren
APPLICANT: McNeill, Patricia Dianne
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Therapy
TITLE OF INVENTION: Hematological Malignancies
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APPLICANT:
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APPLICANT: Algate, Paul A.
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APPLICATION NUMBER: US 60/222,903
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16; Conserv
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Wang, Aijun
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                                                                                                                                                                                                                                                                                                                                   Conservative
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100.0%; Pred. No.
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hes 0;
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Search completed: February
Job time : 1691 secs
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; ORGANISM: Homo sapiens
US-10-154-884B-2901
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CURRENT APPLICATION NUMBER: US/10/154,884B
CURRENT FILING DATE: 2002-05-23
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
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Best Local
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PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
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PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
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APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection,
TITLE OF INVENTION: Hematological Malignancies
                                                                                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                  Local Similarity
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                                                                                                 161 TTTATAAAGCACTCAA
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Pred. No. 1.8e+02;
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Maximum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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seq length: 2000000000
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em_gss_vrt:
em_gss_mam:
em_gss_mam:
em_gss_pro:
em_gss_rod:
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ALIGNMENTS

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AV341547/c
LOCUS
LOCUS
DEFINITION
AV341547 RIKEN full-length enriched, adult male olfactory bulb Mus
musculus cDNA clone 6430522K10 3', mRNA sequence.

AV341547
VERSION
AV341547 GI:6381599
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mus musculus
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
Mus musculus
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
Mus musculus
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
REFERENCE
1 (bases 1 to 211)
Conacs, T., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Kusakabe, M.,
C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata
, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H.,
Matahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T.,
Yoshiki, A., Yoshino, M., Muramateu, M. and Hayashizaki, Y.

TITLE
JOURNAL
Contact: Yoshihde Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic

Result No.

Score

Query Match

Length

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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AV341547 BU465599 AA097151 AQ207356

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Description

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
  BU465599.1
EST.
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                                                                               BU465599 389 bp 1603773567F1 CSEQRBN19 Gallus gallus
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Please visit our web site (http://genome.rtc.riken.go.jp) for
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ilarity 100.0%;
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/lab_host="DH10B"
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/sex="male"
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/strain="C57BL/6J"
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s cDNA clone ChEST710f17 5', mRNA
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Department of Biomolecular Sciences
University of Manchester Institute
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 389)
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                Borges, K.M., Brummet, S.R., S.T., Szasz, J., Ravel, J.,
                                                                                                                  Pyrococcus furiosus
                                                                                                                                                          AA097151.1
EST.
                                                                                                                                                                                               AA097151
                                                                                                                                                                                                                AA097151 394 bp mRNA
0299F Pyrococcus furiosus 1-ZAP II library,
furiosus cDNA clone 0299, mRNA sequence.
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Fax: 01612360409
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                                                        Thermococcaceae; Pyrococcus.
1 (bases 1 to 394)
                                                                                               Archaea; Euryarchaeota;
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., Szasz,J.,
F.T.
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/clone_Torgan: ovary; Vector: pBluescript II KS(+); Site_1:
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Pollowing this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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/clone="ChEST710f17"
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lab_host="DH10B"
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                Bogert, A.,
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                Davis,M.C., Hujer,K.M., Do
,J., Fuller,C., Chase,J.W.
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Pyrococcus furiosus
(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        487 bp DNA linear GSS 18-SEP-1998
HS_3240_B1_G02_T7 CIT Approved Human Genomic Sperm Library D Homo
Bactions genomic clone Plate=3240 Col=3 Row=N, genomic survey
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Amersham Life Science, Inc.
Amersham Life Science, 26101 Miles Rd,
Tel: 2164649277; 4102348870
Fax: 2163600975; 4102348896
                                                                                                                                              High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seat
                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 487)
Mahairas,G.G., Wallace,J.C., Smitl
Keller,A., Shaker,R., Furlong,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996 Contact: Brummet
                                   Plate: 3240 rov
Class: BAC ends
                                                                                                                                                                                                                                                                              Sequence-tagged connectors: A sequence approach to mapping scanning the human genome
                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                              scanning the human genome Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
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                                                                      Sequence Tagged Connector
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138
                                                                                        (206) 616-3618
(206) 616-3887
l: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.3%; Silarity 100.0%; Conservative 0;
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                   quality sequence stop: 487
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/note="Vector: 1-ZAP II; Site 1: Eco RI; Site 2: Eco RI;
Genomic DNA was purified from P. furiosus cells and
partially digested with Dra I, Eco RV, Hinc II, Pvu II,
size selected, ligated to Eco RI linkers then cloned into
the Eco RI site of 1-ZAP II, plasmid excision vector.
Excision was performed in batch and individual clones
retrieved by plating."

93 g 107 t 6 others
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/mol_type="mRNA"
/strain="DSM 3638"
Location/Qualifiers
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                                                                                                                                                  Seattle,
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39;
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Young,J., Zhao,S.,
                                                                                                                                                  WA 98109,
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Gutaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutaryota; Metazoa; Chordata; Galliformes; Phasianidae;
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19; Conserv
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Fax: 01612360409
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Department of Biomolecular Sciences
University of Manchester Institute
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Pong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
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604142968F1 CSEQRBN11 Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: Simon. Hubbard@umist.ac.uk.
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/ Indicate Transcript | I KS(+); Site_1: ECORI; / Clone | Ibb="CSEQRENII" | / Note="Vector: pBluescript II KS(+); Site_1: ECORI; / Note="Vector: pBluescript II KS(+); Site_1: ECORI; / Site_2: Not1; This normalized library was constructed from site of the first sit
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E-Coli DH10B"
a 95 c 153 g 106 t
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="muscle"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="Plate=3240 Col=3 Row=N'
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/strain="Layer and broiler"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="Male and female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="ChEST978h18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Gallus gallus"
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Gallus gallus
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603784821F1 CSEQCHN72 Gallus gallus cDNA clone CheST73915 5', mRNA
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Department of Biomolecular Sciences
University of Manchester Institute
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1 (bases 1 to 672)
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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                                                                  /clone lib="CSEQCHN72"
/clone lib="CSEQCHN72"
/clone lib="CSEQCHN72"
/clone lib="CSEQCHN72"
/clone | Site_2: Not1; This normalized library was
Econstructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996: 791, except that a significantly longer
reannealing hybridization was used."
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone="ChEST73915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             strain="Compton Line"
db_xref="taxon:9031"
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BX165567.1
GSS.
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19; Conserv
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98263205 AGENAE Gallus gallus multi-tissues normalized
once-subtracted cDNA library (gcal) Gallus gallus cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. humquery@sanger.ac.uk Unpublished This sequence was generated from the T7 end of part of the Daniokey BAC Library created by R. Keygene. Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
                                                                                                                          Archosauria; Aves; Neognathae; Galliformes; Pl
Phasianinae; Gallus.
1 (Dases 1 to 679)
Herault,F., Le Meuth-Metzinger,V., Desert,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-MAR-2003) The Sanger Institute, Campus, Hinxton, Cambridgeshire, CB10 1SA, UK.
INRA, UMR INRA-ENSAR Genetique Animale 65, rue de Saint-Brieuc, RENNES cedex, Tel: +33 (0) 2.23.48.54.63
                                                Contact: Douaire M
                                                                Unpublished
                                                                               Construction and primary characterization multi-tissue cDNA libraries
                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                            Gallus gallus (chicken)
Gallus gallus
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                                                                                                                                                                                                                                                            BX263205.1 GI:28585803
                                                                                                                                                                                                                                                                                           gcal0008c.n.07 5prim, mRNA sequence.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
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/db_xref="taxon:7955"
/clone="DKEY-124L1"
/tissue_type="Testis"
/note="vector pindigoBAC-536"
a 120 c 128 g 258 t
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/mol_type="genomic DNA"
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Pred. No. 45;
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                                                                                                                                                                                                                                                                                                  Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishi, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                               Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB621652 RIKEN full-length enriched, 11 days embryo head Mus musculus cDNA clone 6230413013 5', mRNA sequence.
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Sequence cleaned of vector, adaptator and repetitions. Contact us
at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: 0008 row: n column: 7 Seq primer: M13R.
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayateu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                       Unpublished
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/note="Wector: pT73D-pac; tissues: adipose tissue, brain, kidney, liver, multi-tissues, muscle, ovary, testis, bone marrow, caecum, duodenum, embryos, fabricius gland, granulosa, hypothalamus, ileon, jejunum, oviduct, pancreas, skin, spleen, thymus, utero-vaginal gland, pituitary, sakin, spleen, thymus, utero-vaginal gland, pituitary, gland, hematopoietic progenitor cells, small follicle. Clone distribution: AGENAE Resource centre. Francois PIUMI, Francois.Piumi.inra.fr, INRA, CEA Raddibiologie et Etude du genome (LEEG), Domaine de Vilvert, 78352,
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154 c 187 g
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/dev_stage="from_embryos_to_adults"
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sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Pukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
                                                                  BU255698
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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
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further details.
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                                                                                                                                                                                                                                                                                                                       Similarity
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GAGAGAGAGAGAGCTCCTATTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                BamHI."
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nead"
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/dev_stage="11 days embryo"
/lab_host="DH10B"
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  GI:25513312
                                                               698 bp mRNA linear EST 26-NOV-2002 CSEQCHN38 Gallus gallus cDNA clone ChEST657n21 5', mRNA
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Pred. No. 45;
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Best Local Similarity
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Archosauria; Aves; Neognathae; Gall: Phasianinae; Gallus.
1 (bases 1 to 716)
Boardman, P.E., Sanz-Ezquerro, J., Ov. Fong, W.T., Tickle, C., Brown, W.R.A.,
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1 (bases 1 to 698)

1 (bases 1 to 698)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
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Gallus
Gallus
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603473484F1 CSEQCHN70 Gallus
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Gallus gallus
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                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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//clone lib="CERQCHN38"
//clone | Torgan: limbs; Vector: pBluescript II KS(+); Site_1:
//cote="Organ: limbs; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: Not1; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with ECORI
, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-932 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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gallus
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/lab_host="DH10B"
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/clone="ChEST657n21"
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                                                                                                                                                                        GI:25865331
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., E Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., E Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., E Boardman, P.E., Sanz-Ezquerro, J., Wilson, S.A. Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. A Comprehensive Collection of Chicken cDNAs A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002)
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19; Conserv
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                                                                                                                                                                                                                                                                                                                                        Gallus gallus (chicken)
Gallus gallus
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Department of Biomolecular Sciences
University of Manchester Institute
                                        Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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603363138F1 CSEQRBN21 Gallus
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Site 1: EcoRI; Site 2: Not1; This normalized library was
constructed from 1 million independent clones cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996: 791, except that a significantly longer
reannealing hybridization was used."
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/dev_stage="36"
/lab_host="DH10B"
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/strain="White Leghorn,
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Manchester, M60 1QD,
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Tel: 01612008930

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PUBMED
COMMENT
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AUTHORS
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BU378628
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KEYWORDS
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                                                                                   FEATURES
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JOURNAL
MEDLINE
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Best Local
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                                                              source
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                                                                                                                                                                                                                                                                                                                 Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 770)

Boardman, P. E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (chicken)
Gallus gallus
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                                                                                                                                                                                                            Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute
                                                                                                                                                                      PO Box 88, Manchester,
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//lab_host="pH10B"
//clone_lib="CSEQRBN21"
//clone_lib="CSEQRBN21"
//clone_lib="CSEQRBN21"
//note="forgan: ovary; Vector: pBluescript II KS(+); Site_1:
//note="forgan: ovary; Vector: pBluescript Was Looker ovary; Vector: pBluescript Was Looker ovary; Constructed From 1 million independent clones: cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction.

synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction.

Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
                                                                              Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simon.Hubbard@umist.ac.uk.
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/clone="ChEST258k9"
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                 /organism="Gallus gallus"
/mol_type="mRNA"
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/strain="Compton Line 151"
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               type="mRNA"
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; Pred. No.
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llus gallus
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cDNA clone ChEST791g16 5',
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VERSION
KEYWORDS
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BU268139
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MEDLINE
PUBMED
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., E Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. A Comprehensive Collection of Chicken cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 787)
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                                                                                                                                                                                                                                                                          Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                          Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                               PO Box 88, Manchester, Tel: 01612008930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Curr. Biol. 12 (22), 1965-1969 (2002)
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//Clone="Organ: kidney + adrenal; Vector: pBluescript II
//note="Organ: kidney + adrenal; Vector: pBluescript II
KS(+); Site_1: EcoRI; Site_2: Not1; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with EcoRI
, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1995): 791, except that a significantly longer
reannealing hybridization was used."
/dev_stage="22"
/lab host="PH10B"
/clome_lib="CSEQCHN52"
/clome_Tib="CSEQCHN52"
/note="Organ: limbs; Vector: pBluescript II KS(+); Site_1:
ECORI; Site_2: Not1; This normalized library was
constructed_from 1 million independent clones. cDNA
                                                                                                                                                          /organism="Gallus gallus"
/mol type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
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/lab_host="DH10B"
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                                                                                                                                     clone="ChEST428h4"
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                     M60 1QD,
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46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Hubbard, S.J.
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RESULT 15
BU446400
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ORGANISM
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MEDLINE
PUBMED
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603211673F1 CSEQRBN13 Gallus gallus cDNA clone ChEST196b19 5', mRNA
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Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
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Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: Simon. Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BU446400.1 GI:25935711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PO Box 88, Manchester, M60 1QD, UK
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/note=Torgan: Ovary; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: Not1; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS
                                                                                                                                                                                                                                                                                                                                      /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                            /clone="ChEST196b19"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="Layer"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                         clone_lib="CSEQRBN13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ocation/Qualifiers
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유 8

KEYWORDS

VERSION

FEATURES

Query Match Best Local Similarity

8.3%;

Score 19; Pred. No.

DB 13; 47;

COMMENT

TITLE

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REFERENCE
AUTHORS
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BU314014
LOCUS
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ORIGIN
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BASE COUNT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 810)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., E
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A.
A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BU314014 810
603541537F1 CSEQCHN61 Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Biomolecular Sciences University of Manchester Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Simon Hubbard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Simon. Hubbard@umist.ac.uk.
                        ø
                                                                                                                   /note=Torgan: heart; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: Not1; This normalized library was constructed from 1 million independent clones. cDNA synthesis was intiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 pBluescript (KS+) vector. The library was normalized in 2
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186 c 229 g 189 t
                 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research (1996): 791, except that a significantly longer reannealing hybridization was used."

192 c 236 g 194 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        db_xref="taxon:9031"/clone="ChEST511j10"
                                                                                                                                                                                                                                                                                                                                                                              dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               strain="Compton Line 151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Gallus gallus"
                                                                                                                                                                                                                                                                                                                                                                                                         sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:25822015
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                                                                                                                                                                                                                                                                                                                                                               host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _type="mRNA"
                                                                                                                                                                                                                                                                                                                                         lib="CSEQCHN61"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13;
46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Science and Technology (UMIST
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                                                                                  Genome Research 6
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REFERENCE
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                                                             RESULT 18
BU122081
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BZ253924
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VERSION
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                          DEFINITION
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                                                                                                                                                                                                                                                            Query Match
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                    BU122081 850 bp 1603146589F1 CSEQCHL17 Gallus gallus
                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
plate: 499 row: B column: 10
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., OJONG, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BZ253924 833 bp DNA linear GSS 15-OCT-2002
CH230-499B10.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished Other_GSSs: CH230-499B10.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BZ253924.1 GI:23957862
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      sequence.
                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCTCACGGAGTCTGGATT 177
                                                                                                                                           GATGGCCTTAAGTTCCTCT 192
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                                                                                                                                                                                                                       Conservative,
                                                                                                                                                                                                                                                                                                                    Pieter de Jong"
165 c 170 g
                                                                                                                                                                                                                                                                                                                                                         /clone lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
CHORI-230 Rat [BN/S8NHsd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                     /sex="Female"
/cell_type="Brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Rattus norvegicus"
|mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="CH230-499B10"
                                                                                                                                                                                                                                        8.3%;
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                                                                                                                                                                                                                                          Score 19;
Pred. No.
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                                                                                                                                                                                                                                                                                                                          229
                                                                                                                                                                                                                                          DB
47;
                                                                                                                                                                                                                                                            29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MD 20850,
                        cDNA clone ChEST146b24
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                                                                                                                                                                                                                                                            Length 833;
                                                                                                                                                                                                                         Indels
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                      EST 25-NOV-2002
F146b24 5', mRNA
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                 539 TCCTCACGGAGTCTGGATT 557
                                                                                                                                                          sequence.
BU121203
BU121203.1
EST.
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1 (bases 1 to 850)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
Gallus gallus (chicken)
Gallus gallus (chicken)
Gallus gallus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 873)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
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                                                                                                                                                                                                                                            BU121203 873
603003002F1 CSEQCHL17 Gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: Simon. Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simon Hubbard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (chicken)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: kidney + adrenal; Vector: pBluescript II KS(+); Site 1: EcoRI; Site 2: Not1; Modification of pBluescript II KS(+) [Stratagene] vector to accommodate cDNA produced with the T-trimmed protocol (Construction of uni-directionally cloned cDNA libraries from messenger RNA for improved 3' end DNA sequencing by Glenn Fu, et al. U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI. Ligate in double stranded adaptor containing BsgI and BamHI sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [5'ggccgcgtgcagccccggatccgaaaaaaag]
[5'aattctttttttcggatccggggctgcacgc] "
197 c 246 g 208 t
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| lab_host="DH10B"
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db_xref="taxon:9031"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_lib="CSEQCHL17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="ChEST146b24"
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gallus
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47;
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                                                                                                                                                                                                                                            linear EST 25-NOV-2002
one ChEST13c2 5', mRNA
      Burt, D.W., Bosch, E., and Hubbard, S.J.
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Matches
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Tel: 01612008930
Fax: 01612360409
                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (Bases I to 873)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E. Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A. Comprehensive Collection of Chicken cDNAs
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                                                                                                                                                                                                                                                                                                                                               Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BU387613 873 bp mRNA linear EST 28-NOV-2002 603861170F1 CSEQCHN75 Gallus gallus cDNA clone ChEST872117 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Comprehensive Collection of Chicken cDNAs Curr. Biol. 12 (22), 1965-1969 (2002) 22335534
PO Box 88, Manchester, Tel: 01612008930 Fax: 01612360409
                                                                           Department
University
                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (chicken)
                                                                                                                     Contact: Simon Hubbard
                                                                                                                                                                                                                                                                                                                                                                                                        BU387613.1 GI:25895614
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University of Manchester Institute of Science and Technology (UMIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simon Hubbard
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                                                                                                                                          L2445392
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Conservative 0; Mismatches
                                                                                                                                                                            Biol. 12 (22), 1965-1969
                                                                                                                                                                                                                                                                                                                                             gallus
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Clone lib="CSEQCHL17"
//note="Organ: kidney + adrenal; Vector: pBluescript II
KS(+); Site_1: ECORI; Site_2: Not1; Modification of
pBluescript II KS(+) [Stratagene] vector to accommodate
cDNA produced with the T-trimmed protocol (Construction of
uni-directionally cloned cDNA libraries from messenger RNA
for improved 3' end DNA sequencing by Glenn Fu, et al.
U.S. Patent # 6,387,624). Cut pBluescript II KS(+) with
NotI and ECORI. Ligate in double stranded adaptor
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[5'aattcttttttcgggctcgggatccggagc]"
192 c 245 g 227 t
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/clone="ChEST13c2"
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lab_host="DH108"
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'strain="Compton Line 151"
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                                                                           of Biomolecular Sciences of Manchester Institute
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                                     M60 1QD, UK
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48;
                                                                             of Science and Technology (UMIST
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JOURNAL
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Best Local
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              Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
plate: 382 row: K column: 20
Seg_primer: SP6
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BZ255847.1 GI:23961629
GSS.
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19; Conserv
                                                                                                                                                                                                                                       Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                   Contact: Shaying Zhao
Department of Eukaryotic Genomics
Department of Ercharyotic Research
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhao,S., Shetty,J., Shatsman,S., Tsegaye,G., Geer,K., Shvartsbeyn,A., Gebregeorgis,E., Overton,L., Russell,D., Chen,D., Riggs,F., Jong,P. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                  Other_GSSs: CH230-382K20.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CH230-382K20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 873)
                                                                                                                                                                                                                                                                                                                                                                                                                               BAC End Sequences from Library CHORI-230 MboI segment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9323 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="CSEQCHN75"
/note="Organ: trunks; Vector: pBluescript II KS(+);
/note="Organ: trunks; Vector: pBluescript II KS(+);
Site_1: EcoRI; Site_2: Not1; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref="taxon:9031/clone="ChEST872117"
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 943)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
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   Conservative
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                                                                                   /tissue_type="duodenal adenocarcinoma, cell line"
/lab host="NIH MGC 88"
/clone_lib="NIH MGC 88"
/note="Organ: small intestine; Vector: pCMV-SPORT6;
Site_1: Not1; Site_2: Sal1; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."

194 c 230 g 239 t
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/clone_lib="CHORI-230 Segment 2"
/notee="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
/notee="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by
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/db_xref="taxon:9606"
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/clone="CH230-382K20"
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                                                                                                                                                                                                                                                       /clone="IMAGE:4395785"
                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
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19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (12-APR-2000) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Estimate of human gene number provided by using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL190373.1 GI:7828477
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                            genome. For more information, please thttp://www.genoscope.cns.fr/Tetraodon.
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254C04 of library G from Tetraodon
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ilarity 100.0%;
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/note="Genoscope sequence ID :
/note="Genoscope sequence ID :
217 c 195 g 293 t
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/mol_type="genomic_DNA"
/db_xref="taxon:99883"
/clone="254C04"
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           1249
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                                                                                                                                                                                                                                                                                                                      BB562950
238 bp mRNA linear EST 29-NOV-200
BB562950 RIKEN full-length enriched, adult male heart Mus musculus
CDNA clone 1010001C13 5', mRNA sequence.
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High
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 152000 Std Bror: 0.00
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1276)
Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
Warren, W., Graves, T., Mardis, E. and Wilson, R.
Gallus gallus BAC End Reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: Sp6 ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gallus gallus (chicken)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC317416
CC317416.1 GI:30711474
                                                                                                                                                                                                                                                                                              BB562950.1
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                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTATCCTTCCTACTCACT 1267
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Location/Qualifiers
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324 c 197 g 376 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_line="UCD001, inbred 256"
/clone_lib="TAM32"
/notee="Vector: pECBAC1; Site_1: EcoRI; Site_2:
/notee="Vector: pECBAC1; Site_1: for_library_and
TAM32 Female_Chicken library_- for_library_and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="TAM32-27L22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Gallus gallus"
|mol_type="genomic DNA"
for Genome Exploration Research Group, RIKEN Genomic
                                                                                                                                                                                                                                                                                              GI:11453842
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100.0%; Pr
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52;
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URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
Linciperiolic of the property of
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BB564795
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 286)
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
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BB564795.1 GI:11455687
                                                                                                     Mus musculus
                                                                                                                                   Mus musculus (house mouse)
                                                                                                                                                                         EST
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                286 bp mRNA linear EST 29-
RIKEN full-length enriched, adult male stomach Mus
cDNA clone 2200001F22 5', mRNA sequence.
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/db_xref="taxon:10090"
/clone="1010001C13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="adult"
/lab_host="BNN132"
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Pred. No.
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1.2e+02;
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                                                                                                         Local Similarity
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                                                                                     18;
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Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303
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Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki V. and Havsehizki V.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
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                                          AAATTTTTGATGGCCTTA 53
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                                                                                  Conservative
                                                                                                                                                                                                                             prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                          was cleaved with XhoI
74 C 64 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Site_1: XhoI; Site_2: SstI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="stomach"
/dev_stage="adult"
/lab_host="SOLR"
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Pred. No. 1.2e+02;
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63 t
                                                                                                                           Length 286;
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186 CCTCCGTCCCTCCATATT 203
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Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosid
: eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                           sequence.
AL386985
AL386985.1
EST.
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermattoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99AS667 Rice Seedling Lambda (indica cultivar-group) cDNA BE230315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished Contact: Eun M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE230315
BE230315.1 GI:8956640
                                                                                                                             Niebel, A.,
                                                                                                                                              Journet, E.P., Crespeau, H.,
                                                                                                                                                                                                                                                                                        Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                        MtBC39B07F1 MtBC Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: myeun@sun20.asti.re.kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            National Inst. of
Suwon, Kyunggido,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Cytogenetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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e,M.C., Shin,Y.C.,
                                                                                                                                                                     (bases 1 to 473)
                                                                                                          and Gamas, P
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82 331 290 0307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Rice Seedling Lambda ZAPII cDNA Library" /note="Vector: pBluescript SK(+); Site 1: EcoRI; Site XhoI; Directional cDNA library inserted into lambda ZA vector at 5'end with EcoRI and 3' end with XhoI site" a 115 c 103 g 108 t
                                                                                       truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Oryza sativa
/mol_type="mRNA"
/cultivar="Milyang23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:39946"
/clone="99AS667"
                                                                                                                             Carreau, V.,
                                                                                                                                                                                                                                                                                                                                GI:9686736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 18; DB 10;
Pred. No. 1.4e+0;
0; Mismatches (
                                                                                                                         Chatagnier, O.,
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ambda ZAPII cDNA Library Oryza sativa
cDNA clone 99AS667, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                          truncatula cDNA
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tagnier,O., Kahn,D.,
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                                                                                       endomycorrhizal roots
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                                                                                                                                              Gouzy, J., Jaillon, O.,
                                                                                                                                                                                                                                                                                                                                                                                            linear EST 03-AUG-2000
lone MtBC39B07 T3, mRNA
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                                                                                                                             Gianinazzi-Pearson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lambda ZAPII
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KEYWORDS
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BE230459
FEATURES
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                                                                                                                                                          COMMENT
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JOURNAL
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Best Local
                                                                                                                                                                                                                                          AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                Department of Cytogenetics
National Inst. of Agri. Sci. and
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@sun20_asti.re.kr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32
                                                                                                                                                                                                                                                                                 Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNRS-INRA, BP 27 31326 Castanet-Tolosan cedex, rial Mt-est@toulouse.inra.fr Website:
http://sequence.toulouse.inra.fr/Mtruncatula.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE230459
99AS575 Rice Seedling Lambda ZAPII (indica cultivar-group) cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                           BE230459.1
                                                                                                                                                       Contact: Eun M.Y.
                                                                                                                                                                       Darge-scale Sequencing Unpublished
                                                                                                                                                                                                                        Nahm, B.H.
                                                                                                                                                                                                                                               Lee, M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                   (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 2/3 calcined Terragreen mix in the presence of onion root fragments colonized by the arbuscular mycorrhizal fungus Glomus intraradices (Schenck & Smith, isolate LPAB). The plants were watered every day and twice a week with a modified nutrient Long Ashton solution without phosphate but with a high level of nitrate. After 3 weeks RNA was extracted from whole root systems. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zap XR vector from Stratagene and packaged using Gigapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, Evry, France). Note: EST may be of fungal origin."
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                                                                                                                                                                                                                                          ., Shin,Y.C., Lee,T.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=TVector: pBluescript pSK; Site_1: EcoRI; Site_2: XhoI; M. truncatula sterilised seeds were germinated for 72h at 25 C, before transplanting into a 1/3 Epoisses soil
Location/Qualifiers
                                                                                                                                                                                                                                                                   1 to 477)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:3880"
/clone="MtBC39B07"
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cultivar="Jemalong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Medicago truncatula"
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Pred.
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No.
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                                                                                                                                                                                                                                          Jeong, S.H.,
                                                                                                         Tech,
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CDNA Library Oryza sativa
99AS575, mRNA sequence.
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                                                                                                                                                                                                 Rice Seedling
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REFERENCE
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LOCUS
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18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cote, F., Ojanen-Reuths, T., Hahn, M.G., VandenBosch, K., Hur, J., Beremand, P., Endre, G., Town, C.D., Bowman, C.L., Craven, M.B. and Cho, J., Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medicago truncatu
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EST422405 MGHG Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Georgia name: G270678e TIGR sequence name: MTJBA54TK More information is available at: http://chrysie.tamu.edu/medicago Seq primer: SKmod (CTA gAA CTA gtg gAT CC).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Georgia
220 Riverbend Road, Athens, GA 30602-4712,
Tel: 706-542-4457
Fax: 706-542-4412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complex Carbohydrate Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESTs from seedling roots of Medicago truncatula after treatment with beta glucan elicitor preparation from Phytophthora sojae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Medicago truncatula (barrel medic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE942826.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: hahn@ccrc.uga.edu
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/clome="pMGHG-9J11"
/tlssue_type="Roots from four day old seedlings"
/tlssue_type="Roots from four day old seedlings"
/dev_stage="2 days after treatment with beta glucan
/dev_stage="2 days after treatment with beta glucan
/lab host="E. Coli strain XLOLR"
/lab host="E. coli strain XLOLR"
/lab host="E. coli strain XLOLR"
/clome_lib="MGHG"
/clome_lib="MGHG"
/note=""Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="policy bluescript Sk-; Site_1: EcoRI; Site_2: EcoRI; Site_2:
/note="policy bluescript Sk-; Site_1: EcoRI; Site_2: EcoRI; Sit
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/cultivar="Milyang23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .477
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/lab_host="E. coli SOLR"
/clone_lib="Rice Seedling Lambda ZAPII cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:39946"
/clone="99AS575"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               mol_type="mRNA"
cultivar="A17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:10520585
                                                                                                                                                                                                                                                                                                                                                                                                                                   xref="taxon:3880"
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Pred. No. 1.4
0; Mismatches
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1.4e+02;
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RESULT 31
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Best Local
                          ORGANISM
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                                                                                                                                                                               184 TTTTCTATTTCTTGCCTC 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 518)

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J. Maize Genomics Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUEGJ78TD ZM_0.6_1.0_KB genomic survey sequence. CC407239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                          RPCI-23-223H8.TV RPCI-23 genomic survey sequence. AZ700056
                                                                                                                                                                                                                                  18;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
Contact: Cathy Whitelaw
Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                       Mus musculus
                                                  AZ700056.1
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zea mays
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                                                                                                                 AZ700056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays
                                      Mus musculus (house mouse)
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1 68 c 95 g 177 t 2 others
                                                                                                                                                                                                                                                                                            /clone lib="ZM_0.6_1.0 KB"
/note="Vector: pcR4-T9D0; Site_1:
CoT selected genomic DNA library"
104 c 109 g 118 t
                                                                                                                                                                                                                                                                                                                                                /clone="ZMMBTa246M12"
                                                                                                                                                                                                                                                                                                                                                                          /strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               db xref="taxon:4577"
                                                               GI:12421104
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                                                                                                                                                                                                                                           Score 18;
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Pred. No.
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Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                               DB 29; I
1.4e+02;
hes 0;
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                                                                                                     clone
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RPCI-23-223H8,
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AUTHORS
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ORGANISM
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VERSION
KEYWORDS
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CA390726
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PUBMED
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EST.
 Mol. Vis.
22103460
12107410
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18; Conserv
                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                            114
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Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC.
page: http://www.tigr.org/cdb/bac_ends/mouse/bac_end_intro.html
plate: 223 row: H column: 8
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9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Sha, Levins, M., Mcgann, S., Tsegaye, G., Geer, K., and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                     CA390726 548 bp mRNA linear E CB12h07.y1 Human Retinal pigment epithelium/choroid (Un-normalized, unamplified): cs Homo sapiens cDNA cl 5', mRNA sequence.
                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhili; Hominidae; Homo.

1 (Dases 1 to 548)

1 (Dases 1 to 548)

Wistow,G. Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.

Expressed sequence tag analysis of human RPE/Chorold for the NEIBank Project: Over 6000 non-redundant transcripts, novel genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: T7
Class: BAC ends.
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Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Other_GSSs: RPCI-23-223H8.TJ
and splice variants
Mol. Vis. 8 (4), 205-220 (2002)
                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).

103 c 98 g 212 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'db_xref="taxon:10090"
'clone="RPCI-23-223H8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . .527
                                                                                                                                                                                                                                                                                                                                                  GI:24722000
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Pred. No. 1.4
0; Mismatches
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1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens cDNA clone cs112h07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MD 20850,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  end
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VERSION
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
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                                                                                                                                                         JOURNAL
                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                       ORGANISM
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les 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                 AZ399438
AZ399438.1
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Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                     University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1M0165J13F Mouse 10kb plasmid U clone UUGC1M0165J13 F, genomic
                                                                                                                                                                                            Mouse whole genome scaffolding with paired
                                                                                                                                                                                                              Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ399438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: graeme@helix.nih.gov
Plate: 112 row: h column: 07
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                                                  Contact: Robert B.
                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCCTACTCACTGTCCTC 132
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                                                                                                                                                                                                                                                                                            nmalia; Eutheria;
(bases 1 to 550)
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                801 585 5606
801 585 7177
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301 496 0078
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                                                     USA
ddunn@genetics.utah.edu
                                                                                                                                                                         inserts
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chttp://www.invitrogen.com/>). The library code designation was cs. For this library, cDNA inserts were cloned into the NotI/MluI sites of the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Human Retinal pigment epithelium/choroid cDNA (Un-normalized, unamplified): cs"
(Un-normalized, unamplified): cs"
/note="Organ: Eye; Vector: pcMvSPORT6; Two different donor eyes (75-80 years old) yielded approximately 600 mg of dissected RPE/choroid tissue. This in turn yielded 340 ug of total RNA and 7 ug of mRNA. A directionally cloned cDNA library in the pcMvSPORT6 vector was constructed at Life Technologies (Rockville, ND; now part of Invitrogen Corp),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="RPE/choroid"
/dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="cs112h07"
                                                                                                                                                                                                                                                                                                                                                                                                                   GI:10514512
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tive 0;
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                                                                                                                                    Weiss
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%; Pred. No. 1.5
0; Mismatches
                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;
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smid UUGC1M library Mus
                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       survey sequence.
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hes 0;
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                                                                                                                                                                                                                                                                                                                Murinae; Mus.
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[73
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                                                                                                  COMMENT
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RESULT 35
AW687310
LOCUS
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ORGANISM
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KEYWORDS
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Best Local
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                                                                                                                                                                                                                                                                       AUTHORS
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                                                                                                                                                                                                                                                                                                                                  Medicago truncatula (barrel medic)
Medicago truncatula
Medicago truncatula
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
Spermatophyta; Magnoliophyta; eudicotyledons; Trifolieae;
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
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                                                                                                                                                                                     1 (bases 1 to 580)
Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,
Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., M
,G.D. and Paiva,N.L.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
                                                                                 Unpublished
On Apr 14, 2000 this
Contact: Paiva NL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NF008C04RT1F1033 Developing root Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 550.
Location/Qualifiers
                                                                                                                                                                  Medicago truncatula root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AW687310.2 GI:11930471
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with TA DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWH92 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coil XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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/clome_lib="Mouse 10kb plasmid UUGCIM library"
/note="Vector: pWp2ny, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory Mouse DNA Resource
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                                                                                                            sequence version
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Pred. No. 1.5e+0
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                                                                                                                                                                library
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                                                                                                               replaced gi:7562046
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AUTHORS
TITLE
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AUTHORS
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AG242176
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                                                                  BASE COUNT
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Query Match
Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391
                                                                                                                                                                                                                                       Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute The First Laboratory for Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan (B-mail:ssato@kazusa.or:jp, URL:http://www.kazusa.or.jp/en/plant/.Tel:81-438-52-3935(ex.2336), Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  Sato, S., Nakamura, Y. and Tabata, S. Lotus japonicus TAC End sequences Published Only in Database (2002) 2 (bases 1 to 589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lotus japonicus DNA,
AG242176
AG242176.1 GI:26553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: nlpaiva@noble.org
Theart Length: 738 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                   Sato,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lotus japonicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAGAAATTTTTGATGGC 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAGAAATTTTTGATGGC 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="root"
/dev_stage="Pooled developmental"
/dlone_lib="Developing root"
/note="Vector: Lambda Zap; Total RNA was extracted from non-nodulated roots of plants grown in 1 mM nitrate medium. Samples were taken at four time points (approximately two days, one, two and six weeks post germination) representing early seedling growth to nitrogen limitation."

a 94 c 135 g 162 t
                                                                                   /clone="LjT10d14_sf1"
/clone_lib="genomic TAC library"
/note="VECTOR.PYLTAC7"
102 c 59 g 221 t
                                                                                                                                                  /mol_type="genomic DNA"
/strain="Miyakojima MG-20"
/db_xref="taxon:34305"
                                                                                                                                                                                                      organism="Lotus japonicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Medicago truncatula"
/mol_type="mRNA"
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                                  7.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            589 bp DNA clone:LjT10d14_sfi,
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                Score 18;
Pred. No.
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Pred. No.
 Mismatches
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 1.5e+02;
hes 0;
                                DB 29;
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genomic s
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                                Length 589;
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CB934904/c
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ORGANISM
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                                                                                                                                      Query Match
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  25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This library was generated by cloning cDNAs directionally into
Uni-ZAP(Stratagene) (T3 primer/EcoRI are at the 5'-end and T7/XhoI
are at the 3'-end). The library was excised [now in pBluescript
SK(+)] and normalized (Bonaldo et al 1996 Genome Research 6:791-806
). Library constructed by Thomas Baum (tbaum@iastate.edu), Iowa
State University, Plant Pathology Department and Jeff McDermott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heterodera glycines
Heterodera glycines
Eukaryota; Metazoa; Nematoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 601)
McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,
    Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rq98e06.y1
similar to
                                                                                           18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (jpmcderm@iastate.edu).
Seq primer: T3 from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Gibbons, M., Ritter, B., Bennett, J., Franklin, C., Tsagarcishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera
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                                                                                                              Similarity
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                                             TTTGTCCTCCACTTTCAC 226
                                                                                                                                                                                                         127
                                                                                           Conservative
                                                                                                                                                                                                                                           /Glone lib="Heterodera glycines egg"
/note="Vector: pBluescript SK+ (Stratagene); Site 1: XhoI;
Site 2: EcoRI; This library was generated by cloning cDNAs
directionally into Uni-ZAP(Stratagene) (T3 primer/EcoRI
are at the 5'-end and T7/XhoI are at the 3'-end). The
library was excised (now in pBluescript SK+)] and
normalized (Bonaldo et al 1996 Genome Research 6:791-806).
Library constructed by Thomas Baum (tbaum@iastate.edu),
Liowa State University, Plant Pathology Department and Jeff
                                                                                                                                                                                                         McDermott
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:51029"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="whole organism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Heterodera glycines"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            type="mRNA"
                                                                                                              100.0%;
                                                                                                                                                                                                    (jpmcderm@iastate.edu)."
194 g 124 t
                                                                                        <u>,,</u>
                                                                                                              Pred. No.
                                                                                        red. No. 1.5
Mismatches
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                                                                                        DB 14; I
. 1.5e+02;
:hes 0;
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Heterodera glycines cDNA
[1] ;, mRNA sequence.
                                                                                                                                    Length 601;
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VERSION
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AUTHORS
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CA922246/c
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AF074623/c
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Best Local
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                                                                                                                                                                                                                                                                                              32
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CA922246
Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                         655
AF074623 Human fetal liver cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medicago truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid.
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                Ha0156, mRNA sequence.
AF074623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR sequence name: MTUBY29TV
More information is available at: www.medicago.
Seq primer: (gtA AtA CgA CtC ACt AtA ggg C).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 612 624 2755
Fax: 612 625 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VandenBosch, K., Endre, G., Silversteir
Utterback, T., Cheung, F. and Fraser, C.
The Medicago truncatula 6K unigene se
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EST639964 MTUS Medicago truncatula
                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA922246.1
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                                                        fomo sapiens (human)
                                                                                                                                                                                                                                                                                  TCAGAAATTTTTGATGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                          216
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="MTUS"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."

135 c 86 g 197 t
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/dev_stage="various stages"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Medicago truncatula"
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clone="MTUS-51C5"
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                                                                                              GI:6470442
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                                                                                                                                                                                                                                                                                                                                                  Score 18;
Pred. No.
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     Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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library
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1.5e+02;
thes 0;
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                                                                                                                                                                                                                                                                                                                                                                     Length 634;
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JOURNAL COMMENT
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AI110716/c
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Department of Hematology
Beijing Institute of Radiation Medicine
27 Taiping Road, Beijing 100850, P.R.China
Tel: 0086-10-68159479
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                                                                                                                                                                                                          Beijing Institute of Radiation Medicine
27 Taiping Road, Beijing 100850, P.R.Ch
                                                                                                                                                                                                                                      Contact: Yongtao Yu
Department of Hematology
                                                                                                                                                                                                                                                                    Unpublished
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                                                                                                                                                                                                                                                                                                           Yu, Y
                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 655)
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HA0156 Human fetal liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: yyt48@yahoo.com
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                                                                                                                                                                   Email: yyt48@yahoo.com
                                                                                                                                                                                  Fax: 0086-10-68214653
                                                                                                                                                                                             Tel: 0086-10-68159479
                                                                                                                                                                                                                                                                                Expression profile analysis of a human fetal liver cDNA library
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                                                                                                                                                                                                                                                                                                          Zhang, C., Luo, L.,
                                                    /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="liver"
/dev_stage="fetal"
/lab_host="MC1061/p3"
                           /clone lib="Human fetal liver cDNA library"
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/lab_host="MC1061/P3"
/clone_lib="Human_fetal_liver_cDNA_library"
/note="Vector: pCDNA1"_____
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/db_xref="taxon:9606"
/clone="Ha0156"
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Lotus japonicus
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Loteae,
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
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                                                                    Eukaryota, Viridiplantae, Streptophyra, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD clade, Panicoideae, Andropogoneae, Zea.

1 (bases 1 to 665)
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    Nakamura, Y. and Tabata, S. japonicus TAC End sequences shed Only in Database (2002)

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/note="WECTOR:PYLTAC7"
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Myler, P.J., Vogt, C., Munden, H., Robertson, L., Sisk, E., Faze, Aggarwal, G., Nelson, S., Seyler, A., Worthey, E., Stuart, K.
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Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                  Seq primer: SP6
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                              Other_GSSs: LB00548a.d_T7.1
Contact: Myler PJ
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                                                                                                                                                                                                                                                                                                                   Email: mylerpj@sbri.org
                                                                                                                                                                                                                                                                                                                                        Tel: 206 284-8846
Fax: 206 284-0313
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/clone lib="ZM2 0.7 1.5 kB"
/note="Wector: pBCSK; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
a 116 c 108 g 189 t
/clome lib="Leishmania major Friedlin BAC Library" /clome lib="Leishmania major Friedlin | Commic DNA from /note="Vector: pCG270; Site 1: HindIII; Genomic DNA from Leishmania major Friedlin in agarose blocks was partially digested with HindIII, size selected, and ligated with HindIII-digested pCG270 vector DNA. 1036s clomes were picked and arrayed in 384- and 96-will plates. Library construction and arraying was carried out by ResGen
                                                                                                                                                                                     /organism="Leishmania major"
/mol_type="genomic DNA"
/strain="Friedlin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="B73"
/db_xref="taxon:4577"
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                                                                                                                                   lab_host="E. coli GeneHogs +
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1.5e+02;
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CA922247/c
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Medicago truncatula
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More information is available at:
Seq primer: (gtA AtA CgA CtC ACt I
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 704)
VandenBosch,K., Endre,G., Silverstein,K, Town,C.D., Van Aken,S.,
Utterback,T., Cheung,F. and Fraser,C.M.
The Medicago truncatula 6K unigene set: cDNA clones selected and
re-arrayed from various libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 612 624 2755
Fax: 612 625 1738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: kvandenb@cbs.umn.edu
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                        TCAGAAATTTTTGATGGC
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                                                                                                                                                /clone lib="MTUS"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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                                                                                                                                                                                                                                                                                                       /tissue_type="mixed tissues"
/dev_stage="various stages"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:3880"
clone="MTUS-51C6"
                                                                                                                                                                                                                                                                                                                                                                                           cultivar="A17"
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hes 0;
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AtA ggg C).
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Clone distribution: MGC clone distribution information can clone distribution: MGC clone distribution information can clone distribution.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="retinoblastoma"
/lab host="DH10B (phage-resistant)"
/clome_lb="NIH_MGC_16"
/clome_lib="NIH_MGC_16"
/clome_lib="NIH_MGC_16"
/clome_lib="NIH_MGC_16"
/clomed_into_EccRI/XhoI sites using the following 5'
cloned_into_EccRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library_constructed_by_Ling_Hong_
in_the_laboratory_of_Gerald_M. Rubin (University_of_California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript_II RT (Life_Technologies).
Note: this is a NIH_MGC_Library."
25 a 176 c 206 g 200 t
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/db_xref="taxon:9606"
/clone="IMAGE:4634083"
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